

ACTGACCTCGGTTCTATCGATTGAATTCCTCCCGGGATCCTCTAGAGATCCCTCGACCTCGA
 CCCACGCGTCCGGGCCGGAGCAGCACGGCCGCAGGACCTGGAGCTCCGGCTCGCTCTCCCG
 CAGCGCTACCCGCCATGCGCCTGCCGCGCCGGCCGCGCTGGGGCTCCTGCCGCTTCTGCTG
 CTGCTGCCGCCCGCGCCGGAGGCGGCCAAGAAGCCGACGCCCCGCCACCGGTGCCGGGGCT
 GGTGGACAAGTTTAAACAGGGGATGGTGGACACCGCAAAGAAGAACTTTGGCGCGGGAAACA
 CGGCTTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCTGCTGGAGATC
 CTGGAGGGGGCTGTGCGAGAGCAGCGACTTCAATGCAATCAGATGCTAGAGGCGCAGGAGGA
 GCACCTGGAGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCTGACTTATTGAGTGGTTTT
 GTGTGAAGACACTGAAAGTGTCTGCTCTCCAGGAACCTACGCTCCCGACTGTCTCGCATGC
 CAGGGCGGATCCAGAGGCCCTGCAGCGGAATGGCCACTGCAGCGGAGATGGGAGCAGACA
 GGGCGACGGGTCTGCGCGGTGCCACATGGGGTACCAGGGCCCGCTGTGCACTGACTGCATGG
 ACGGCTACTTTCAGCTGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCC
 TGCAAGACGCTGCGGCCTGACCAACAGACAGAGCTGCGCGCAGTGTGAAGTGGGCTGGGTGCT
 GGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAGTCCGCTCCCTCGACGCGCT
 CGCAGTTCTGTAAGAACGCCAACGGCTCCTACAGCTGCGAAGAGTGTGACTCCAGTGTGTG
 CGCTGCACAGGGGAAGGCCCCAGGAACCTGTAAGAGTGTATCTCTGGCTACGCGAGGGAGCA
 CGGACAGTGTGCAGATGTGGACGAGTGTCTCACTAGCAGAAAAAACCTGTGTGAGGAAAAACG
 AAAACTGCTACAATACTCCAGGGAGTACGTCTGTGTGTCTCTGACGCGTTTCAAGAAACG
 GAAGATGCTGTGTGCCGCCGGCAGAGGCTGAAGCCACAGAAGGAGAAAGCCCGACACAGCT
 GCCCTCCCGGAAGACCTGTAATGTGCCGGACTTACCCTTTAAATTATTGAGAAGGATGTCC
 CGTGGAAAATGTGGCCCTGAGGATGCCGTCTCCTGCAGTGGACAGCGCGGGGAGAGGCTGC
 CTGCTCTCTAACGGTTGATTCTCATTTGTCCCTTAAACAGCTGCATTCTTGTTGTCTTTA
 AACAGACTTGTATATTTTGATACAGTTCTTTGTAAATAAAATTGACCAATTGTAGGTAATCAGG
 AGGAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAGAGTCGACCTGCAGAAGC
 TTGGCCGCCATGGCCCAACTTGTTTTATTGCGACTTATAATGGTTACAAATAAAGCAATAGCA
 TCACAAATTTACAAATAAAGCATTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAAACTC
 ATCAATGTATCTTATCATGTCTGGATCGGAATTAATTCGGCGCAGCACCATGGCCTGAAAT
 AACCTCTGAAAGGAACTTGGTTAGGTACCTTCTGAGGCGGAAAGAACCAGCTGTGGAATG
 TGGTTCAGTTAGGTTGTGAAAGTCCCCAGGCTCCCAGCAGGCAGAGTATGCAAGCATGC
 ATCTCAATTAGTCAGCAACCAAGCTTTT

FIGURE 2

><subunit 1 of 1, 353 aa, 0 stop
><MW: 38192, pI: 4.53, NX(S/T): 2
MRLPRRAALGLLPLLLLLPPAPEAAKPTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAWEKTL SKYESSSEIRL
LEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFCVKT LKVCSPGT YGPDCLACQGGSGRQPCSG
NGHCSGDGSRQGDGSCRCHMGYQGPLCTDCMDGYFSSLRNETHS ICTACDESCKTC SGLTNRDCGECEVGWVLDE
GACVDVDECAAEPPPCSAAQFCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLAEKT
CVRKNENCYNTPGSYVVCVCPDGFEETEDACVPPAEAEATEGESPTQLPSREDL

Signal peptide:

amino acids 1-24

N-glycosylation sites.

amino acids 190-194 and 251-255

Glycosaminoglycan attachment sites.

amino acids 149-153 and 155-159

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 26-30

Casein kinase II phosphorylation sites.

amino acids 58-62, 66-70, 86-90, 197-201, 210-214, 255-259, 295-299, 339-343
and 349-353

Tyrosine kinase phosphorylation site.

amino acids 303-310

N-myristoylation sites.

amino acids 44-50, 54-60, 55-61, 81-87, 150-156, 158-164, 164-170, 252-258 and
313-319

Aspartic acid and asparagine hydroxylation site.

amino acids 308-320

EGF-like domain cysteine pattern signature.

amino acids 166-178

Leucine zipper pattern.

amino acids 94-116

FIGURE 3

CAGGTCCAAC TGCACCTCGGTTCTATCGATTGAATTCCCGGGGATCCTCTAGAGATCCCTC
GACCTCGACCCACGCGTCCGCCAGGCCGGGAGGCGACGCCCCAGCCGTCTAAACGGGAACA
GCCCTGGCTGAGGGAGCTGCAGCGCAGCAGAGTATCTGACGGCGCCAGGTTGCGTAGGTTGCG
GCACGAGGAGTTTTCCCGGCAGCGAGGAGGTCTGAGCAGCAGTGGCCCGGAGGAGCGCCTTC
CCTGCCGCCGCGCTCTGGCTCTGGAGCATCCTCCTGTGCCTGCTGGCACTGCGGGCGGAGGC
CGGGCCGCCGAGGAGGAGAGCCTGTACCTATGGATCGATGCTCACCGGCAAGAGTACTCA
TAGGATTTGAAGAAGATATCCTGATTGTTT CAGAGGGGAAAAATGCGACCTTTTACACATTTGAT
TTCAGAAAAGCGCAACAGAGAATGCCAGCTATTCTGTCAATATCCATTCATGAATTTTAC
CTGGCAAGCTGCAGGGCAGGCAGAACTACTCTATGAATTCCTGTCTTGGCTCCCTGGGATA
AAGGCATCATGGCAGATCCAACCGTCAATGTCCCCTCTGCTGGGAACAGTGCTCACAAGGCA
TCAGTTGTTC AAGTTGGTTTCCCATGTCTTGAAAAACAGGATGGGGTGGCAGCATTTGAAGT
GGATGTGATTGTTATGAATTTCTGAAGCAACACCATTCTCCAACACCTCAAATGCTATCT
TCTTTAAACATGTCAACAAGCTGAGTGCCAGGCGGGTGCCGAAATGGAGGCTTTTGTAAT
GAAAGACGATCTGCGAGTGTCTGATGGGTTCCACGGACCTCACTGTGAGAAAGCCCTTTG
TACCCACGATGTATGAATGGTGGACTTTGTGTGACTCCTGGTTTCTGCATCTGCCACCTG
GATTTCTATGGAGTGAAGTGTGACAAAAGCAAACCTGCTCAACACCTGCTTTAATGGAGGGACC
TGTTTCTACCTGGAAAAATGTATTTGCCCTCCAGGACTAGAGGGAGAGCAGTGTGAAATCAG
CAAATGCCCAACACCTGTGCAAAATGGAGGTAAATGCATTTGGTAAAGCAAATGTAAGTGT
CCAAAGGTTAC CAGGGAGACCTCTGTTCAAAGCCTGTCTGCGAGCCTGGCTGTGGTGCCAT
GGAACCTGCCATGAACCAACAAATGCCAATGTCAAGAAGGTTGGCATGGAAGACACTGCAA
TAAAGGTACGAAGCCAGCCTCATACATGCCCTGAGGCCAGCAGGCGCCAGCTCAGGCAGC
ACAGCCCTTCACTTAAAAAGGCCGAGGAGCGCGGGATCCA CTGAATCCAATTACATCTGG
TGA ACTCCGACATCTGAACCGTTTAAAGTTACACCAAGTTTATAGCCTTTGTTAACCTTTCA
TGTGTTGAATGTTCAAATAATGTTTATTACACTTAAGAATACTGGCTGAATTTTATTAGCT
TCATTATAAATCACTGAGCTGATATTTACTCTTCTTTTAAAGTTTCTAAGTACGCTGTAG
CATGATGGTATAGATTTTCTGTTTCAGTGCTTTGGGACAGATTTTATATTATGTCAATTGA
TCAGGTTAAATTTT CAGTGCTGATTTGGCAGATATTTCAAATTA CAATGCATTTATGGT
GTCTGGGGGCAGGGGAACATCAGAAAGGTTAAATGGGCAAAATGCGTAAGTCAACAAGAT
TTGGATGGTGAGTTAATGTTGAAGTTACAGCATTT CAGATTTTATGTGATATTTAGAT
GTTTGTGTACATTTTAAAAAATTGCTCTTAATTTTAAACTCTCAATACAATATATTTTGACC
TTACCATTATTC CAGAGATTCAGTATTA AAAAAAAAAAAAAATTACACTGTGGTAGTGGCATT
AAACAATATAATATA TTTCAAACACAATGAAATAGGGAATATAATGTATGAACCTTTTGTGAT
TGCTTGAAGCAATATAATATATTTGTAACAAAACACAGCTCTTACCTAATAAACATTTTAT
ACTGTTTGTATGTATAAAATAAGGTGCTGCTTTAGTTT TTTGGAAAAA AAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAGGCGCGCAGCTCTAGAGTCGACTGCAGAGCTTGGC
CGCCATGGCCCACTGTTTATTG CAGCTTATAATG

FIGURE 4

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33094
><subunit 1 of 1, 379 aa, 0 stop
><MW: 41528, pI: 7.97, NX(S/T): 2
MARRSAFPAAALWLWSILLCLLALRAEAGPPQEESLYLWIDAHQARVLIGFEEDILIVSEGK
MAFFTTHDFRKAQQRMPAIPVNIHSMNFTWQAAGQAEYFYEFSLRSLDKGIMADPTVNVPLL
GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPPGGC
RNGGFCNERRICECPDGFHGPHEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCST
TCFNGGTCFYPGKCICPPGLEGEQCEISKCPQPCRNGGKCIGKSKCKCSKGYQGDLCSKPVC
EPGCGAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAERRDP
• PESNYIW
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Signal peptide:

amino acids 1-28

N-glycosylation site.

amino acids 88-92, 245-249

Casein kinase II phosphorylation site.

amino acids 319-323

Tyrosine kinase phosphorylation site.

amino acids 370-378

N-myristoylation sites.

amino acids 184-190, 185-191, 189-195, 315-321

ATP/GTP-binding site motif A (P-loop).

amino acids 285-293

EGF-like domain cysteine pattern signature.

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

FIGURE 5

CGGACGCGTGGGCGTCCGGCGGTGCGCAGAGCCAGGAGGCGGAGGCGCGCGGGCCAGCCTGGG
CCCCAGCCCACACCTTCACCAGGGCCCAGGAGGCCACCAATGTGGCGATGTCCACTGGGGCTAC
TGCTGTTGCTGCCGCTGGCTGGCCACTTGGCTCTGGGTGCCCAGCAGGGTCTGGGGCGCCGG
GAGCTAGCACCGGGTCTGCACCTGCGGGGCGATCCGGGACGCGGGAGGCGCGTACTGCCAGGA
GCAGGACCTGTGCTGCCGCGGCGTGCAGCAGACTGTGCCCTTACCTGGGCGCCATCT
GTTACTGTGACCTCTTCTGCAACCGCACGGTCTCCGACTGTGCCCCGACTTCTGGGACTTC
TGCTCGGCGTGCCACCCCTTTTCCCCGATCCAGGATGTATGCATGGAGGTCTGATCTA
TCCAGTCTTGGGAACGTACTGGGACAACTGTAACCGTTGCACCTGCCAGGAGAACAGGCAGT
GGCATGTGTGATCCAGACATGATCAAAGCCATCAACCAGGGCAACTATGGCTGGCAGGCTGG
GAACACAGCGCCTTCTGGGGCATGACCCCTGGATGAGGGGCATTTCGCTACCGCCTGGGCACCA
TCCGCCCCTCTTCCGCTCATGAACATGCATGAAATTTATACAGTCTGAAACCCAGGGGAG
GTGCTTCCCACAGCCTTCGAGGCCTCTGAGAAAGTGCCCAACCTGATTCATGAGCCTCTTGA
CCAAGGCAACTGTGCAGGCTCCTGGGCCTTCTCCACAGCAGCTGTGGCATCCGATCGTGTCT
CAATCCATTCTTGGGACACATGACGCTGTCTGTGCGCCCCAGAACCTGTCTGTCTTGTGAC
ACCCACCAGCAGCAGGGCTGCCGCGGTGGGCGTCTCGATGTGTGCTGGTGTCTGCGCTCG
CCGAGGGGTGGTGTCTGACCACTGCTACCCCTTCTCGGGCGGTGAACGAGACGAGGCTGGCC
CTGCGCCCCCTGTATGATGCAAGCCGAGCCATGGGTGCGGGCAAGCGCAGGCCACTGCC
CACTGCCCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCTGTCTACCGCCT
CGGCTCCAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCA
TGGAGGTGCAATGAGGACTTCTTCTATACAAGGGAGGCATCTACAGCCACACGCCAGTGAGC
CTTGGGAGGCCAGAGAGATACCGCGGGCATGGGACCCACTCAGTCAAGATCACAGGATGGGG
AGAGGAGACGCTGCCAGATGGAAGGACGCTCAAATACTGGACTGCGGCCAACTCCTGGGGCC
CAGCCTGGGGCGAGAGGGGCCACTTCCGCATCGTGCGCGCGCTCAATGAGTGCGACATCGAG
AGCTTCGTGCTGGGCGCTTGGGGCCGCTGGGCATGGAGGACATGGGTCACTACTGAGGCTG
CGGGCACCACGCGGGGTCCGGCTGGGATCCAGGCTAAGGGCCGGCGGAAGAGGCCCAATG
GGGCGGTGACCCAGCCTCGCCGACAGAGCCCGGGGCGCAGGCGGGCGCCAGGGCGCTAAT
CCCGGCGCGGTTCCGCTGACGCGAGCCTCCGCTGGGAGCCGCGGGCAGGCGAGACTGGCG
GAGCCCCCAGACCTCCAGTGGGGACGGGGCAGGGCCTGGCCTGGGAAGAGCACAGCTGCAG
ATCCAGGGCCTCTGGCGCCCCACTCAAGACTACCAAAGCCAGGACACTCAAGTCTCCAGC
CCCAATACCCACCCCAATCCCGTATTCTTTTTTTTTTTTTTTAGACAGGGTCTTGCTCCG
TTGCCAGGTTGGAGTGAGTGGCCCATCAGGGCTCACTGTAACCTCCGACTCCTGGGTTCA
AGTGACCTCCCACTCAGCCTCTCAAGTAGCTGGGACTACAGGTGCAACCCACACCTGGC
TAATTTTGTATTTTGTAAAGAGGGGGTCTCACTGTGTTCGCCAGGCTGGTTTCGAACT
CCTGGGCTCAAGCGGTCCACCTCGCCTCCCAAGTGCTGGGATGCAGGCATGAGCC
ACTGCACCCAGCCTGTATTCTTATTCTTCAGATATTATTCTTTTCACTGTTTTAAAA
TAAACCAAAGTATTGATAAAAAAAA

CGGACGCGTGGGCGTCCGGCGGTGCGCAGAGCCAGGAGGCGGAGGCGCGCGGGCCAGCCTGGG

FIGURE 6

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223

><subunit 1 of 1, 164 aa, 1 stop

><MW: 18359, pI: 7.45, NX(S/T): 1

MWRCPLGLLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYCQEQLCCRGRADDC
ALFYLGAICYCDLFCNRTVSDCCPDFWDFCLGVPPFPFPIQGCMMHGRIYFVLGTYWDNCNR
CTCQENRQWHGGSRHDQSHQPGQLWLAGWEPQRLLGHDPG

N-glycosylation site.

amino acids 78-82, 161-165

Casein kinase II phosphorylation site.

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,
411-415

N-myristoylation site.

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,
269-275, 378-384, 442-448

Amidation site.

amino acids 26-30, 318-322

Eukaryotic thiol (cysteine) proteases histidine active site.

amino acids 398-409

FIGURE 7

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FIGURE 9

MTHRTTTWARRTSRAVTPTCATPAGPMPCSRLLPPSLRCSLHSACCSGDPASYRLWGAPLQPT
LGVVVPQASVPLLTDLAQWEPVLVPEAHFNASLTMYVCTPVPHDPMPMALSRTPTTRQISSSDT
DPPADGFSNPLCCCFHGPAPFSTLNFVLRHLFPQEAFPAHPIYDLSQVWSVVSPAPSRGQALRRAQ

Signal peptide:

amino acids 1-47

N-glycosylation site.

amino acids 31-35, 74-78, 84-88

Casein kinase II phosphorylation site.

amino acids 22-26, 76-80

N-myristoylation site.

amino acids 56-60

Amidation site.

amino acids 70-74

FIGURE 10

CCCACGCGTCCGAACCTCTCCAGCG**ATGGG**GAGCCGCCCGCTGCTGCCAACCTCACTCTGT
GCTTACAGCTGCTGATTCTCTGTGTCAAACCTAGTACGTGAGGGACCAGGGCGCCATGACC
GACCAGCTGAGCAGGCGGCAGATCCGCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCA
CGTGCAGGTCAACCGGGCTCGCATCTCCGCCACCGCCGAGGACGGCAACAAGTTTGGCCAAGC
TCATAGTGGAGACGGACAGTCTTGGCAGCCGGGTTCGCATCAAAGGGGCTGAGAGTGAGAAG
TACATCTGTATGAACAAGAGGGGCAAGCTCATCGGAAGCCCAGCGGGAAGAGCAAAGACTG
CGTGTTACGGAGATCGTGCTGGAGAACAATAACGGCCTTCCAGAACGCCCGGCACGAGG
GCTGGTTCATGGCCTTCACGCGGCAGGGGCGGCCCGCCAGGCTTCCCGCAGCCGCCAGAAC
CAGCGCGAGGCCCACCTTCATCAAGCGCCTCTACCAAGGCCAGCTGCCCTTCCCCAACCACGC
CGAGAAGCAGAAGCAGTTTCGAGTTTGTGGGCTCCGCCCCACCCGCCGACCAAGCGCACAC
GGCGGCCCCAGCCCTCAC**AGT**CTGGGAGGCAGGGGGCAGCAGCCCTGGGCCGCCCTCCC
CACCCCTTTCCTTTTAATCCAAGGACTGGGCTGGGGTGGCGGGAGGGGAGCCAGATCCCC
GAGGGAGGACCCTGAGGGCCGCGAAGCATCCGAGCCCCAGCTGGGAAGGGGAGGCCGGTG
CCCCAGGGGCGGCTGGCACAGTGCCCCCTTCCCGGACGGGTGGCAGGCCCTGGAGAGGAACT
GAGTGTACCCCTGATCTCAGGCCACCAGCCTCTGCCGGCTCCAGCCGGGCTCCTGAAGCC
CGCTGAAAGGTCAGCGACTGAAGGCCTTGCAGACAACCGTCTGGAGGTGGCTGTCTCTAAAA
TCTGCTTCTCGGATCTCCCTCAGTCTGCCCCAGCCCCCAAACCTCTCTGGCTAGACTGTA
GGAAGGGACTTTTGTCTTGTCTTGTCTTTCAGGAAAAAAGAAAGGGAGAGAGAGGAAATAG
AGGGTTGTCCACTCTCACATTCACGACCCAGGCCTGCACCCACCCCCAACTCCAGCCC
CGGAATAAAACCATTTTCTCTGC

FIGURE 11

MGAARLLPNLTLCQLLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRI
SATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNKRGLIGKPSGKSKDCVPTTEIVLE
NNYTAFQNAHHEGWFMFAFTRQGRPRQASRSRQNRQEAHFIAKRLYQGQLPFPNHAQKQKQFEF
VGSAPTRRTKRTRRPQPLT

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 9-13, 126-130

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 60-64

Casein kinase II phosphorylation site.

amino acids 65-69

Tyrosine kinase phosphorylation site.

amino acids 39-48, 89-97

N-myristoylation site.

amino acids 69-75, 188-194

Amidation site.

amino acids 58-62

HBGF/FGF family signature.

amino acids 103-128

FIGURE 12

ACTTGCCATCACCTGTTGCCAGTGTGGAAAAATTCTCCCTGTTGAATTTTTCGCATGGAG
GACAGCAGCAAAGAGGGCAACACAGGCTGATAAGACCAGAGCAGCAGGGAGATTATTTTAC
CATACGCCCTCAGGACGTTCCCTCTAGCTGGAGTTCTGGACTTCAACAGAACCCCATCCAGT
CATTTTGATTGTGCTGTTTATTTTTTTTTCTTTTCTTTTCCACCACATTGTATTTTAT
TTCCGTACTTCAGAAATGGGCTACAGACCACAAAGTGGCCAGCCATGGGGCTTTTTCCT
GAAGTCTTGGCTTATCATTTTCCCTGGGGCTCTACTCACAGGTGTCCAAACTCCTGGCCGTGC
CTAGTGTGTCGCCGTGCGACAGGAACCTTTGTCTACTGTAATGAGCGAAGCTTGACCTCAGTG
CCTCTTGGGATCCCGGAGGGCGTAACCGTACTCTACCTCCACAACCAAAATTAATATGC
TGGATTTCTGCGAAGTGCACAATGTACAGTCGGTGCACACGGTCTACCTGTATGGCAACC
AACTGGACGAATTCCCCATGAACCTTCCCAGAAATGTGAGAGTCTCCCATTTGCGAGGAAAAC
AATATTGAGACCATTTCCAGGGCTGCTCTTTGCCAGCTCTTGAAGCTTGAAGAGCTGCACCT
GGATGACAACCTCCATATCCACAGTGGGGGTGGAAGACGGGGCTTCCGGGAGGCTATTAGCC
TCAAATTGTTGTTTTTGTCTAAGAATCACCTGAGCAGTGTGCTGTTGGGCTTCTGTGGAC
TTGCAAGAGCTGAGAGTGGATGAAAATCGAATTGCTGTCATATCCGACATGGCCCTCCAGAA
TCTCAGAGCTTGGAGCGTCTTATTGTGGACGGGAACCTCCTGACCAACAAGGGTATCGCCG
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CACCCCTCCTCCGATCTCCAGGTACGCATCTGATCAGGCTCTATTTGCGAGGACAACCAGAT
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ACAACCAACTGCGGATGTGACTCAAGGGGTTTTTGATAATCTCTCAAACCTGAAGCAGCTC
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CCTCTCTTCAACCCAGCCCCAAGTACAGCTTCTCCGACCACTCAGCCTCCACCTCTCTAT
TCCAAACCTTAGCAGAAGCTACACGCCTCCAACTCCTACCACATCGAAACTTCCACGATTC
CTGACTGGGATGGCAGAGAAAGAGTGACCCACCTATTTCTGAACGGATCCAGCTCTCTATC
CATTTTGTGAATGATACTTCCATTCAGTCAGCTGGCTCTCTCTCTTACCCTGATGGCATA
CAAACCTCACATGGGTGAAAATGGGCCACAGTTTAGTAGGGGGCATCGTTGAGGAGCGCATAG
TCAGCGGTGAGAAGCAACACCTGAGCCTGGTTAACTTAGAGCCCCGATCCACCTATCGGATT
TGTTTAGTGCCACTGGATGCTTTTAACTACCGCGCGGTAGAAGACACCACTTTGTTGAGAGG
CACCACCCATGCCTCTATCTGAACAACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGA
CGTCCCACAGCATGGGCTCCCCCTTCTGCTGGCGGGCTTGATCGGGGGCGCGGTGATATT
GTGCTGGTGTCTTGTCTAGCGTCTTTTGTGCGCATATGCACAAAAGGGGCGCTACACCTC
CCAGAAGTGGAAATACAACGGGGCGGGCGGAAAGATGATTATGCGAGGCGAGGCCAACGA
AGGACAACTCCATCCTGGAGATGACAGAAACAGTTTTTCAGATCGTCTCCTTAATAACGAT
CAACTCCTTAAAGGATTTTACAGCTGCAGCCCATTTACACCCCAATGGGGGCATTAAATTA
CACAGACTGCCATATCCCCAACAAATGCGGATATGCAACAGACAGCGTGCAGACCTGGAGC
ACTGCCATACGTGACAGCCAGAGGCCAGCGTTATCAAGGCGGACAAATTAGACTCTTGAGAC
CACACTCGTGTGTGCACATAAAGACACGCAGATTACATTTGATAAATGTTACACAGATGCAT
TTGTGCAATTGAATACTCTGTAATTATACGGGTGACTATATAATGGGATTTAAAAAAGTG
CTATCTTTCTATTTCAAGTTAATTACAAACAGTTTTGTAACTCTTGCTTTTTAAATCTT

FIGURE 13

MGLQTTKWP SHGAFFLKSWLIISLGLYSQVSKLLACPSVCRNDFVYCNERSLTSVPLGIP
EGTVLVLYLHNNQINNAGFP AELHNVQSVHTVYLYGNQLDEFFPMNLPKNVRVLHLQENNIQTI
SRAALAQLLKLEELHLDNDSISTVGVEDGAFREAI SLKLLFLSKNHLSSVPVGLPVDLQELR
VDENRIAVISDMAFQNLTSERLIVDGNLLTNKGIAEGTFSHLTKLKEFSIVRNSLSHPPPD
LPGTHLIRLYLQDNQINHIPLTAFSNLRKLERLDISNNQLRMLTQGVFDNLSNLKQLTARNN
PWFCDCSI KWVTEWLKYIPSSLNVRGFMCCQGPQVRGMVRELNMNLLSCTTTPGLPLFTP
APSTASPTTQPPTLSIPNPSRSYTPPTPTTSKLPTIPDWDGRRVTPPI SERIQLSIHVND
TSIQVSWLSLFTVMAYKLTWVKMGHSLVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVPL
DAFN YRAVEDTICSEATTHASYLNNGSNTASSHEQTTSHSMGSPFLLAGLIGGAVIFVLVVL
LSVFCWHMHKKGRYTSQKWYNRGRRKDDYCEAGTKKDNSILEMTETSFQIVSLNNDQLLKG
DFRLQPIYTPNGGINYTDCHIPNNMRYCNSSVVPDLEHCHT

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 542-561

N-glycosylation site.

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

Casein kinase II phosphorylation site.

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

Tyrosine kinase phosphorylation site.

amino acids 319-328

N-myristoylation site.

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,
522-528, 545-581, 633-639

Amidation site.

amino acids 581-585

Leucine zipper pattern.

amino acids 164-186

Phospholipase A2 aspartic acid active site.

amino acids 39-50

FIGURE 14

ACTTGGAGCAAGCGGCGCGGAGACAGAGGCCAGAGCCAGAAGCTGGGGCTCCGTCTCGCCTCCACGAGCG
ATCCCCGAGGAGAGCGCGGCGCCTCGGCGAGGCGAAGAGGCGACGAGGAGAACCCGGGTGGCTGCGCCCTGCC
TGCCTTCCAGGCGCGCGGCGCTGCAGCCTTGCCCTCTTGCTCGCCTTGAAAATGGGAAAAGATGCTCGCAGGCT
GCTTTCTGCTGATCTCTGGACAGATGCTCTCTCCCTCGCGAGGCGAGGCGGTACGTTGGGAGGTCCATCT
CTAGGGGCGACACAGCTCGAGCCACCCGACAGCGGCCCTTCTGGAGAGTTCTCTGAGAACAGCGGCGAGACC
TGTTTTTCATCATTTGACAGCTCTCGCAGTGTCAACACCCATGACTATGCAAAGGTCAAGAGTTTATCGTGGGAC
TCTTGCATCTTTTGACACTTGGTCTCTGATGTCACCGAGTGGGCCCTGCTCCATATGGCAGCACTGTCAAGAAATG
AGTTCTCCCTCAAGACCTTCAAAGGAAAGTCCGAGGTTGGAGCGTGTGTCAAGAGGATGGCGCATCTGTCCACGG
GCACCATGACTCGGCTGGCCATGAGTATGCCCCGAAACATCGCATTTCTCAGAAAGCAGAGGGGGCCCGGCCCTTGA
GGGAGAAATGTGCCACGGGTATATATGATCGTGACAGATGGGAGACCTCAGGACTCCGTGGCCGAGGTGGCTGCTA
AGGCACGGGACCGGCACTCTTAATCTTTGCCATTTGGTGTGGGCCAGGTAGACTTCAACACCTTTGAAGTCCATTG
GGAGTGAGCCCCATGAGGACCATGTCTTCTTTGGGCCAATTTCAAGCCAGATTGAGACGCTGACCTCCGTGTTCC
AGAAGAAGTTGTGCACGGCCACATGTGCAGCACCTGGAGCATAACTGTGCCCATCTCTGCATCAACATCCCTG
GCTCATACGCTGCAGGTTGAAACAGGCTACATTTCTCAACTCGGATCAGACGACTTGCAGAAATCCAGGATCTGT
GTGCCATGGAGGACCAACTGTGAGCAGCTCTGTGTGAATGTGCCGGGCTCCTTGTCTGCCAGTGCTACAGTG
GCTACGCCCTGGCTGAGGATGGGAAGAGGTGTGTGGCTGTGACTACTGTGCCATCAAGAAACCCAGGATGTGAAC
ATGAGTGTGTAATCTGTATGGCTCTTACCTTTGGCAGTGCCATGAAGGATTTGCTTGAACCATGAAAGAA
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AGCAGGACCATGGCTGTGAGCAGCTGTGTGAAACAGGAGGATTCCTTGTCTGCCAGTGTCTCAGAAGGCTCTC
TCATCAACGAGGACCTCAAGACCTGCTCCCGGGTGGATTAATGCTGCTGTGAGTGACCATGGTTGTGAATACCTCT
GTGTCAACATGGACAGATCTTTTGCTGTCACTGCTCTGAGGACACGCTGCTCCGACGAGTGGGAAGCAGCTGTG
CAAAATTTGGACTCTTGTGCTCTGGGGGACACGGTTGTGAACATTCGTGTGAAGCAGTGAAGATTCGTTTGTGT
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ACCATGGCTGTGAACACATTTGTGTGAACAGTGAACATCATACACAGTGCAGTGCTGTGAGGGATCCCGGCTG
CTGAGGATGGGAACGCTGCCGAAGGAAGGATGTCTGCAAAATCAAACCCACATGGCTGCGAACACATTTGTGTTA
ATAATGGGAATTCCTACATCTGCAAAATGCTCAGAGGGATTTGTTCTAGCTGAGGACGGAAGACGCTGCAAGAA
GCACTGAAGGGCCCAATGGACTGGCTTTGTGTGATCGATGGATCCAAAGATCTTGGAGAGAGAAATTTTGAAGTGT
TGAAGCACTTTGCTACCTGAAATATATAGATTCCTTGACAAATTTCCCAAGCCGCTCGAGTGGGGCTCTGCTCAGT
ATTCCACACAGGTCCACACAGAGTTCACTCTGAGAAATTCACATCAGCCAAAGACATGAAAAAAGCGCTGGGCC
ACATGAAATACATGGGAAAGGGCTCTATGACTGGGCTGGCCCTGAACACATGTTTGAAGAGATTTTATCCCAAG
GAGAGGGCCGAGGCCCCCTTTCCCAAGGGGTGCCAGAGCAGCCATTTGTTTCAACGACGAGCGGGCTCAGGATG
ACGCTCCGAGTGGGCCAGTAAGAACCAAGGCCAATGGTATCACTATGCTATGCTTGGGCTAGGAAGAGCCATGT
AGGAGGAATCTACAAGAGATTTGCTCTGAGGCCACAAACAGCATTCTTCTATGCGGAAGACTCTCAGCACAAATGG
ATGAGATAAGTGAAAAATCAAGAAAGCATCTGTGAAGCTCTAGAAGACTCCGATGGAAGACAGGACTCTCAG
CAGGGGAATCGCAAAAACCGTCCAAACGCCAACAGAATCTGAGCCAGTCAAGATAAATATCAAGAGCTACTTT
CTGTTCTAATTTTGCAGTCAACACAGATATCTGTTTGAAGAGAGCAATCTTTTACGGTCTACACAAAAGCTTT
CCCATTCAACAAAACCTTCAGGAAGCCCTTTGGAAGAAAAACAGCATCTTGTGATCAAGGATTTAATAATGT
TCCAGAACCTTTGCAACGAAGAAATGAAGAAATTAACACAGCGCTTAGAAGAAATGACACAGAGAAATGGAAGCCC
TGGAAATCGCCTGAGATAACAGTGAAGATTAGAAATCGCGACACATTTGTGATCAAGGATTAACAT
GAACGCTGCGAGGCCCAAGGCTCAGGCTATTTGTTAAATCAATATGTTGTGAAGTAAAAACATCAGTACTGA
GAAACCTGGTTTGGCAAGAAACAGAGACAGAGATATACATACTTTGATATAAATTTATCTAGAAAAAAAATCCT
TCAGAATTTCAAGATGAATTTACAGGTTGAGATGAATAAGCTATGCAAGGATTTTGTAAATATATCTGTGGACAC
AATCTGCTTCTGCTCATCTGCTTTAGTTGCAATCTATTGACTATGATTTGCAAGATTTGCAAGCTTTTACT
CTGTAGAACACTGGCCATAGAAATGTCTGTTTTTTTGTACTGCACTTACCTTGATATATGATATGATGTATG
CATAAATCATAGGACATATGACTTTGTGGAACAAGTTGGATTTTTATACAAATTAATAATTCACCACTGAG

FIGURE 15

MEKMLAGCFLLILGQIVLLPAEARERSRGRSISRGRHARTHPTALLESSENKRADLVFI
DSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSKTKFRKSEVERAV
KMRHLSTGTMGLAIQYALNIAFSEAEGARPLRENVPRVIMIVTDGRFPQDSVAEVAAKARD
TGILIFAIGVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSVVFQKKLCTAHMCSTLEHN
CAHFCINIPGSSVYCRCKQGYILNSDQTTCRIQDLCAMEDHNCQLCVNVPGSFVCQCYSGYA
LAEDGKRCVAVDYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCRINICALNKPGC
EHECVNMEESSYYCRCHRGYTLDPNGKTC SRVDHCAQQDHGCEQLCLNTEDSFVCQCSEGLI
NEDLKTCSRVDYCLLSDHGCEYSVCVNMDRSFACQCPGHHVLRSDGKTC AKLDSALGDHGCE
HSCVSSSEDSFVCQCFEGYILREDGKTCRRKDCQAIDHGCEHICVNSSDYSYCECLEGFRLA
EDGKRCRRKDVCKSTHHGCEHICVNNGNSYICKCEGFLAEDGRRCKCTEGPIDLVFVID
GSKSLGEBENFEVVKQFVTGIIDSLTISPKAARVGLLQYSTQVHTEFTLRNFNSAKDMKKAVA
HMKYMGKGSMTGLALKHMFERSFTQEGARPLSTRVPRAAIVFTDGRAQDDVSEWASKAKAN
GITMYAVGVGKAIEBELQBIASEPTNKHLYAEDFSTMDIEISEKLKKGICEALESDGRQDS
PAGELPKTVQQPTSESEPTVINIQDLLSCSNFAVQHRYLFEBDNLLRSTQKLSHSTKPSGSPL
EEKHDQCKCENLIMQNLANEVVRKLTQRLEEMTQRMEALENRLRYR

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 221-225

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 115-119, 606-610, 892-896

Casein kinase II phosphorylation site.

amino acids 49-53, 118-122, 149-153, 176-180, 223-227, 243-247,
401-405, 442-446, 501-505, 624-628, 673-677, 706-710, 780-784,
781-785, 819-823, 866-870

N-myristoylation site.

amino acids 133-139, 258-264, 299-305, 340-346, 453-459, 494-500,
639-645, 690-696, 752-758, 792-798

Amidation site.

amino acids 314-318, 560-564, 601-605

Aspartic acid and asparagine hydroxylation site.

amino acids 253-265, 294-306, 335-347, 376-388, 417-423, 458-464,
540-546, 581-587

FIGURE 16

GGAGCCGCCCTGGGTGTGAGCGGCTCGGCTCCCGCGCAGCTCCGGCCGTCGCGCAGCCTCG
GCACCTGCAGGTCGGTGCCTCCCGGGCTGGCGCCCCCTGACTCCGTCCCGGCCAGGGAGGGC
CATGATTTCCTCCCGGGGCCCCCTGGTGACCAACTGTGTCGGTTTTTTGTTCCTGGGGCTGA
GTGCCCTCGCGCCCCCTCGCGGGCCAGCTGCAACTGCATTGCCCCCAACCGGTTGCAG
GCGGTGGAGGGAGGGGAAGTGTGCTTC CAGCGTGGTACCTTGCACGGGGAGGTGTCTTC
ATCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAGAAAAGGAGGATC
AGGTGTTGTCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTATCCTTGGTCTACTCC
ATGCCCTCCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGAAAGACTCTGGCCCCTA
CAGCTGCTCCGTGAATGTGCAAGACAAAACAAGGCAAATCTAGGGGCCACAGCATCAAAACCT
TAGAACTCAATGTACTGGTTCTCCAGCTCCTCCATCCTGCCGTCTCCAGGGTGTGCCCCAT
GTGGGGCAAAACGTGACCCTGAGCTGCCAGTCTCCAAGGAGTAAGCCCGCTGTCCAATACCA
GTGGGATCGGCAGCTTCCATCCCTCCAGACTTCTTTGCACCAGCATTAGATGTGATCCGTG
GGTCTTTAAGCCTCACCAACCTTTCGTCTTCCATGGCTGGAGTCTATGTCTGCAAGGCCAC
AATGAGGTGGGCACTGCCCAATGTAATGTGACGCTGGAAGTGAGCACAGGGCCTGGAGCTGC
AGTGGTTGTCTGGAGCTGTTGTGGGTACCCTGGTTGGAAGTGGGGTGTCTGGCTGGGCTGGTTC
TCTTGTAACACCGCCGGGGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCC
ATTGCTCCCCGACCCTGCCCTGGCCCAAGAGCTCAGACACAATCTCCAAGAATGGGACCCT
TTCCTCTGTACCTCCGACGAGCCCTCCGGCCACCCCATGGCCCTCCAGGCCCTGGTGCAT
TGACCCCAAGCCAGTCTCTCCAGCCAGGCCCTGCCCTCACCAGACTGCCACGACAGAT
GGGGCCACCCCTCAACCAATATCCCCCATCCCTGGTGGGGTTTTCTTCTCTGGCTTGAGCCG
CATGGGTGCTGTGCTGTGATGGTGCCTGCCAGAGTCAAGCTGGCTCTCTGGTATTGATGAC
CCCACCACTCATTGGCTAAAGGATTTGGGGTCTCTCCTTCTCTATAAGGGTCACCTCTAGCAC
AGAGGCCTGAGTCATGGGAAAGAGTCACACTCCTGACCCCTAGTACTCTGCCCCCACCTCTC
TTTACTGTGGGAAAACATCTCAGTAAGACCTAAGTGTCAGGAGACAGAAGGAGAAGAGGA
AGTGGATCTGGAATTGGGAGGAGCCTCCACCACCCCTGACTCCTCCTTATGAAGCCAGCTG
CTGAAATTAGCTACTCACCAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCAGGC
CCCCTTGATCTGTACCCCAACCCCTATCTAACACCACCCCTGGCTCCCACTCCAGTCCCTGT
ATTGATATAACCTGTGAGCTGGCTGGTTAGGTTTTTACTGGGGCAGAGGATAGGGAATCTC
TTATTAATAACATGAAATATGTGTTGTTTTTCATTGCAAATTTAAATAAAGATACATAA
TGTTTGTATGAAAAA

FIGURE 17

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEVSS
SQPWEVFPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSRLLEGLQEKGDSGPY
SCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSQCQSPRSKPAVQYQ
WDRQLPSFQFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLEVSTGPGAA
VVAGAVVGTLLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWKSSDTISKNGTL
SSVTSARALRPPHGPPRGALTPTPSLSSQALPSPRLPTTDGAHPQPISSIPGGVSSSGLSR
MGAVPVMVPAQSQAQSLV

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 245-267

N-glycosylation site.

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

N-myristoylation site.

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,
262-268, 308-314, 363-369, 364-370

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 164-175

FIGURE 18

CGCCACCAGTGCGGCCACCGCCAATGAAACGCCTCCGCTCCTAGTGGTTTTTCCACTTTG
TTGAATTTGTTCTCTATCTCAAAATTCACCAAGACACCTTGTCTCCCAAATGC AAAATGTGA
AATACGCAATGGAATTGAAGCCTGCTATTGCAACATGGGATTTTCAGGAAATGGTGTCAAA
TTTTGTGAAGATGATAATGAATGTGGAATTTAACTCAGTCCTGTGGCGGCAAAATGGCTAAATTCG
ACTAACACAGGAAGGAAGTTATTATTGTATGTGTGTAACCTGGCTTCAGATCCAGCAGTAAACCA
AGACAGGTTTTATCATAATGATGGAACCGTCTGTATAGAAAATGTGAATGCACCACTGCCATT
TAGATAATGCTGTGTATAGCTGCAAATATTAAATAAACTTTAAACAAAATCAGATCCATAAAA
GAACCTGTGGCTTTGCTACAAGAAAGCTCTATAGAAAATCTGTGACAGATCTTTTCACCAACAGA
TATAATTACATATATAGAAAATATTAGCTGAATCATCTTCATTACTAGGTTACAAGAACAAACA
CTATCTCAGCCAAGGACACCCCTTTCTAACTCAACTCTTACTGAATTTGTA AAAACCGTGAAT
AATTTTGTTCAAAGGGATACATTTGTAGTTTGGGACAAAGTTATCTGTGAATCATAGGAGAAC
ACATCTTACAAAACCTCATGCACACTGTTGAACAAGCTACTTTAAGGATATCCAGAGCTTCC
AAAAGACCACAGAGTTTGATACAAATTCACCGGATATAGCTCTCAAAGTTTTCTTTTGTGAT
TCATATAACATGAAACATATTCATCCTCATATGAATATGGATGGAGACTACATAAATATATT
TCCAAAGGAAAAAGCTGCATATGATTCAAATGGCAATGTTGCAGTTGCATTTTATATTATA
AGAGTATTGGTCTTTGCTTTTCATCATCTGCACAACCTCTTATTGAAACCTCAAAATTTATGAT
AATCTGAAGAGGAGGAAAAAGTTCATATCTTCAGTAATTTTCAGTCTCAATGAGCTCAAAACCC
ACCCACATTTATATGAATCTGAAAAAATAACATTTACATTAAGTCAATCGAAAGGTCACAGATA
GGTATAGGAGTCTATGTGCATTTTGGAAATTACTACCTGATACCATGAATGGCAGCTGGTCT
TCAGAGGGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTATACCT
GACACATTTTGCATTTTGTGATGTCCTCTGGTCTTCCATTGGTATTAAGATTATAAATATTC
TTACAAGGATCACTCAACTAGGAATAATTATTTCACTGATTGTCTTGCCATATGCATTTT
ACCTTCTGGTTTCTCAGTGAATTCAAAGCACCAGGACAACAATTCACAAAAATCTTTGCTG
TAGCCTAATTTCTGCTGAACCTGTGTTTTCTGTGTGGGATCAATACAAATCAATAAAGCTGT
TCTGTTCAATCATTTGCCGAGCTGCTACACTACTTCTTTTTAGTGTCTTTTGCATGGATGTGC
ATTGAAGGCATACATCTCTATCTCATTTGTGTGGGTGTCTCTACAACAAGGGATTTTGGCA
CAAGAAATTTTATATCTTTGGCTATCTAAGCCAGCCGTGGTAGTTGGATTTTCCGACAGCAC
TAGGATACAGATATTATGGCACAACCAAAGTATGTTGGCTTAGCACCGAAAAACAACCTTTATT
TGGAGTTTTATAGGACCAGCATGCTAATCATTTCTGTGAATCTCTGGCTTTTGGAGTCAT
CATATACAAAGTTTTTCTGCACACTGCAGGGTTGAAACCAGAAGTTAGTTGCTTTGAGAACA
TAAGGCTGTGTGAAGAGGAGCCCTCGCTCTTCTGTTCCTTCTCGGCACCACCTGGATCTTT
GGGTTCTCCATGTTGTGCACGCATCAGTGGTTACAGCTTACCTCTACAGTCAAGCAATGC
TTTTCCAGGGGATGTTCAATTTTTTATCTCTGTGTGTTTATCTGAAGAAGATCAAGAAGAAT
ATTACAGATTGTTCAAAATGTCCTGTGTTGTTTGGATGTTAAGGTAACATAGAGAATG
GTGGATAATTACAACCTGCACAAAAATAAAAAATTCCAAGCTGTGGATGACCAATGTATAAAAA
TGACTCATCAAAATTCAAATTATTAACTACTAGACAAAAAGTATTTTAAATCAGTTTTTTCT
GTTTATGCTATAGGAACGTGTAGATAATAAGGTAAAAATTATGTATCATATAGATATACTAGT
TTTTCTATGTGAATAGTTCTGTCAAAAATAGTATTGCAGATATTGGAAGTAATTGGTTTT
CTCAGGAGTGAATACCTGCACCCCAAGGAAAGATTTTTCTTCAACACGAGAAGTATATGAA
TGTCCGTAAGGAAACCACTGGCTTGATATTTCTGTGACTCGTGTGCTTTGAACTAGTCC
CCTACCACCTCGGTAAATGAGCTCCATTACAGAAAGTGGAACATAAGAGAATGAAGGGGAGAGA
ATATCAACAGTGAAGAGGGAATGATAAGATGTTATTGAAAGTGAACCTGTTTTTCTGTAGAC
TAGCTGAGAAATGTTGACATAAAAAATAAGAAATGAAGAAACACATTTTACCATTTTGTGAA
TTGTTCTGAACTTAAATGTCCACTAAAAACAACCTTAGACTTCTGTTTGCTAAATCTGTTCTT
TTTTCTAATATTCTAAAAAAAAGGTTTTACCTCACAATTTGAAAAAAAAGGAAAAA
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FIGURE 19

MKRLPLLVVFSTLLNCSYTONCTKTPCLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDNEC
GNLTQSCGENANCTNTEGSYYCMCVPGFRSSSNQDRFITNDGTVCIEENVNANCHLDNVICAA
NINKTLTKIRSIKEPVALQEVYRNSVTDLSPTDIITYIEILAESSSLGKYKNNTISAKDTL
SNSLTLEFVKTVNNFVQRDRTFVVWDKLSVNHRRTHLTKLMHTVEQATLRISQSFOKTEFDT
NSTDIALKVFFDYSYNNMKHIHPHMNDGDYINIFPKRKAAYDSNGNVAFAFLYYKSIGPLLS
SSDNFLLKPQNYDNSEEEERVISSVISVSMSSNPPTLYELEKITFTLSHRKVTDYRSLCAF
WNYSPDTMNGSWSSSEGCELTYSNETHTSCRCNHLTHFAILMSSGSPSIGIKDYNILTRITQLG
IIISLICLAICIFTWFFPSEIQSTRTTIHKNLCCSLFLABLVLVFGINTNTNKLFCSTIAGL
LHYFFLAAPAWMCIEGIIHLYLIVGVYIYNGKFLHKNFYIFGYLSPAVVVGFSAAALGYRYGT
TKVCWLSTENNFIWSFIGPACLIILVNLLAFGVIIYKVRHTAGLKPEVSCFENIRSCARGA
LALLFLLGTTWIFGVLHVHASVVTAYLFTVSNAFQGMFIFLFLCVLSRKIQEYYRLFKNV
PCCFGCLR

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 430-450, 465-486, 499-513, 535-549, 573-593, 619-636,
648-664

N-glycosylation site.

amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181,
188-192, 249-253, 381-385, 395-399

Glycosaminoglycan attachment site.

amino acids 49-53

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 360-364

Casein kinase II phosphorylation site.

amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154,
155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329,
346-350, 608-612

Tyrosine kinase phosphorylation site.

amino acids 36-44, 669-677, 670-678

N-myristoylation site.

amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394,
434-440, 480-486, 521-527

Aspartic acid and asparagine hydroxylation site.

amino acids 75-87

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GCTCCAGCCAGAACCTCGGGGGCGCTGCGCGGTGGGGAGGAGTTCCTCCGAAACCCGGCCGCTAGCGAGGCTCTCTCTCCGCGAGATCCGAACCGGCTTGGGCGGGGTCACCCCGGCTGGGA
CAAGAAGCCGCGCCTGCTGCTGCCGGGC CGGGGAGGGGGCTGGGGCTGGGCGCGAGGCGG
GGTGTGAGTGGGTGTGTGTGCGGGGGGCGGAGGCTTGATGCAATCCCGATAAGAAATGTCTCGGG
TGCTTTGGGCACCTTCCCGTGGGGCCCGTAAGGCGCTACTATAAAGCTGCGGCGCCGAG
CCGCGCGCGCGTCAGAGCAGGAGCGTGCCTCGAGGATCTAGGGCCACGACCATCCCAACC
GGCATCTCAGCGCCGCGAGGAGTCCCGGTGCGCCGCCAGCTCCCGCACCCCATCTCGCCGG
AGCTCGCCGAGAGCCGCCAGGAGGTGCCATCGGAGCGGGTGTGTGGTGTCTCAGTATG
ATCTTGGCCGGCTCTGGCTGGGCGTGGCGGGGCCCTCGCCTTCTCGGACGCGGGGCC
CCAGCTGCATCAGCGCTGGGGCGACCCCATCTCGCCTCGGGCACTGTGTACACTCCGCGCCCC
ACGGGCTCTCCAGCTGCTTCTGCGCATCGTGCGACGCGGCTGTGGATCTGCGCGGGGG
CAGAGCGCGCACAGTTTGTCTGAGATCAAGGCGATCGCTCTCGGACGCGGGCATCAAGGG
CGTGCAACAGCGTGCGTGCTACCTCTGCATGGGCGCGGCAAGATGACGGGGCTGCTTCAGT
ACTCGGAGGAAGATGTGCTTTCTGAGGAGGAGATCCGCGCGAGATGGCTACAATGTGTACGA
TCCGAAGAAGCACGCTCTCCGCTCTCCTGACGAGTGCACAAACAGCGGCAGCTGTACAAGAA
CAGAGGCTTTCTTCTCACTCTCTCATTTCTGCGCCATGTGCCCATGGTCCAGAGGAGCTG
AGGACCTCAGGGGCCATCTGGAATCTGCATGTTCTTCTCGCCCCGTGGAGACCGACGAGCATG
ACCCATTGTGGGCTGTGCACGGGATCGAAGGCGGTGAGGAGTCCACGCTTGTAGAAAGTAAC
GAGACCATGCGGGGCTCTTCACTGCTGCCGGGGCTGTGGTCTGCTGACGCTGGGGGACG
TGCTTCTACAAGAACAGTCTTGAGTCCACGTTCTGTTTACGCTTTAGGAAGAAACATCTAGAA
GTTGTGATATATCAGAGTTTTCATTTGGCAGTCCGAGTTTCTAGCCCAATAGACTGTCTGAT
ATAACATATGTAAAGCTGTAGCTTGCCAGCTGCTGCTGGGGCCCCATTTGCTCCTCGA
GGTTGCTGGAACAGCTCTGCATGTCTCAGTTCTGATTTGAATACCTCCATCGATGGGGAAC
TCACTTCTTTGAAAAAATCTTATGTCTCAAGCTGAAATTTCTAATTTTTCTCATCACTT
CCAGGAGCAGCCGAGAAGA CAGG CAGTAGTTTAAATTT CAGGAA CAGGTGATCCATCTGTA
AAACAGCAGGCTAAATTTCTACCAACCAATGTGGGAATTGATCTATATCTCTACTCTCAGG
ACCAATTTGCCCTTCCAAATCCTTCAGGCGAAGTCACTGAGCAGGACATGGCCACAG
GCTTCAGGAGTAGGGGAAGCTGTGAGCCCACTCCAGCCCTGGGACAACTTGAGAATTCCTCC
CTGAGGCGAGTTCTGTATGATGATGTGCTCTGAGAATAATTTGCTGTCCCGGTGTCACTGT
TTTCATCTCCAGGCCACACCGCCTTGCCCACTCATAGCTCCCCATGGATGGGGCT
CCCAGGCCCCCACTTATGTCAACCTGCACTTCTTGTTCAAATAACAGGAAAAGAAAAGAT
TTGAAGACCCCAAGTCTGTCAATAACTTGCTGTGTGGAGCAGCGGGGGAAGACCTAGAAC
CCTTTCCCGAGCATGTGGTTTCTCAACATGATATTTATGAGTAATTTATTTTGATGTACA
TCTCTATTTTCTTACATATTTATGCCCCAAATTATATTTATGTATGATGAGGTTTG
TTTTGTATATTAAATGGAGTTTGTGTTGT

FIGURE 22

MRSGCVVHVWILAGLWLAVAGRPLAFSDAGPHVHYGWGDPIRLRHLYTSGPHGLSSCFLRI
RADGVVDCARGQSAHSLLLEIKAVALRTVAIKGVHSVRYLCMGADGKMQGILLQYSEEDCAFEE
EIRPDGYNVYRSEKHRLPVSLSAKQRQLYKNRGFLPLSHFLPMLPMVPEEFEDLRGHLESD
MFSSPLETDSMDPFGLVTGLEAVRSPSF EK

Signal peptide:

amino acids 1-22

Casein kinase II phosphorylation site.

amino acids 78-82, 116-120, 190-194, 204-208

N-myristoylation site.

amino acids 15-21, 54-60, 66-72, 201-207

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 48-59

FIGURE 23

CCCAGAAGTTCAAGGGCCCCGGCCTCCTGCGCTCCTGCCGCCGGGACCTCGACCTCCTCA
 GAGCAGCCGGCTGCCGCCCCGGGAAGATGCGCAGGAGGAGCCGCCACCGCCTCCTCCTGCTG
 CTGCTGCGCTACCTGGTGGTCGCCCTGGGCTATCATAAGGCCTATGGGTTTTCTGCCCCAAA
 AGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTTAGCCTGCAAAACCCCAA
 AGAAGACTGTTTTCTCCAGATTAGAGTGGAAGAACTGGGTCGGAGTGTCTCCTTTGTCTAC
 TATCAACAGACTCTTCAAGGTGATTTTAAAAATCGAGCTGAGATGATAGATTCAATATCCG
 GATCAAAAAATGTGACAAGAAGTGATGCGGGGAAATATCGTTGTGAAGTTAGTGCCCCATCTG
 AGCAAGGCCAAAACCTGGAAGAGGATACAGTCACTCTGGAAGTATTAGTGGCTCCAGCAGTT
 CCATCATGTGAAGTACCCTCTTCTGCTCTGAGTGGAACGTGGTAGAGCTACGATGTCAAGA
 CAAAGAAGGGGAATCCAGCTCCTGAATACACATGGTTTAAGGATGGCATCCGTTTGCTAGAAA
 ATCCCAGACTTGGCTCCCAAAGCACCAACAGCTCATACACAATGAATACAAAACTGGAAC
 CTGCAATTTAATACTGTTTCCAAACTGGACACTGGAGAAATATTCCTGTGAAGCCCGCAATTC
 TGTTGGATATCGCAGGTGTCTGGGAAACGAATGCAAGTAGATGATCTCAACATAAGTGGCA
 TCATAGCAGCCGTAGTAGTTGTGGCCTTAGTGATTTCCGTTTGTGGCCTTGGTGTATGCTAT
 GCTCAGAGGAAAGGCTACTTTTCAAAGAAACCTCCTTCCAGAAGAGTAATTCTTCATCTAA
 AGCCACGACAATGAGTGAAAATGTGCAGTGGCTCACGCCTGTAATCCCAGCACTTTGGAAGG
 CCGCGCGGGCGGATCACGAGGTGAGGAGTTCTAGACCAGTCTGGCCAATATGGTGAACCC
 CATCTCTACTAAAAATACAAAAATTAGCTGGGCATGGTGGCATGTGCCTGCAGTTCAGCTGC
 TTGGGAGACAGGAGAATCACTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCTGAGATCACGC
 CACTGCAGTCCAGCCTGGGTAAACAGAGCAAGATTCATCTCAAAAAATAAAATAAATAAATA
 AATAAATACTGGTTTTTACCTGTAGAATTCTTACAATAAATATAGCTTGATATTC

00001532 101210 3330000

FIGURE 24

MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKTVSSRLE
WKKLGRSVSFVYYQQTLOQDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLLED
TVTLEVLVAPAVPSCCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQST
NSSYTMNTKTGTLOQFNTVSKLDTGEYSCEARNVSGYRRCPGKRMQVDDLNISGIIAAVVVVA
LVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENVQWLTPVIPALWKAAGGSRGQEF

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 130-144, 238-258

N-glycosylation site.

amino acids 98-102, 187-191, 236-240, 277-281

Casein kinase II phosphorylation site.

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

N-myristoylation site.

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

Amidation site.

amino acids 226-230

FIGURE 25

GACATCGGAGGTGGGCTAGCACTGAACTGCCTTTTCAAGACGAGGAAGAGGAGAGAAAG
AAAGAAGAGGAAGATGTTGGGCAACATTTATTTAACATGCTCCACAGCCCGACCTTGGCAT
CATGCTGCTATTTCCTGCAAACTACTGAAGAAGCATGGGATTTAAATATTTTACTTCTTAAATAA
ATGAATTACTCAATCTCTATGACCATCTATACATACTCCACCTTCAAAAAGTACATCAATA
TTATATCATTAAAGGAAATAGTAACCTTCTCTTCTCCAATATGTCATGACATTTTGGACAATG
CAATTTGTGGCACTGGCATTATTTTCAGTGAAGAAAACTTTGTGGTCTTATGGCATTTCATCA
TTTGACAATGCAAGCATCTTCTCTTATCAATCAGCTCCTATTGAACCTTACTAGCAGCTGACTG
TGGAATCCTTAAGGGCCCATACATTTCTGAAGAAGAAAGCTAAGATTGAAGGACATGCCACT
CCGAATTCATGTGCTACTTGGCCTAGCTATCACTACACTAGTACAGCTGTAGATAAAAAAG
TGGATTTGCCAGGTTATGTACGTGTGAAATCAGGCCCTTGGTTTACACCCAGATCCATTTAT
ATGGAAGCATCTACAGTGGATTGTAATGATTTAGGTCTTTTAACTTTCCAGCCAGATTGCC
AGCTAACACACAGATTCTTCTCTACAGACTAACAAATTTGCAAAAATTTGAATACTCCACAG
ACTTTCCAGTAAACCTTACTGGCCTGGATTTATCTCAAAACAATTTATCTTTCAGTCACCAAT
ATTAATGTAAAAAGATGCCCTCAGCTCCTTTCTGTGTACCTAGAGGAAAAACAACCTTACTGA
ACTGCTCGAAAAATGTCTGTCCGAACCTGAGCAACTTACAAGAACCTCTATATTAATCACAAC
TGCTTTCTACAATTTCACTGGAGCCTTATTGGCCTACATAATCTTCTCGACTTTCATCTC
AATTCAAATAGATTGCAGATGATCAACAGTAAGTGGTTTGATGCTCTTCCAATCTAGAGAT
TCTGATGATTTGGGAAAAATCCAATTATCAGAATCAAAGACATGAACCTTTAAGCCTCTTATCA
ATCTTTCGAGCCTGGTTATAGCTGGTATAAACCTCAGAGAAATACCAGATAACGCCCTTGGTT
GGACTGGAACCTTAGAAGCATCTCTTTTACGATAACAGGCTTATTAAAGTACCCCATGT
TGCTCTTCAAAAAGTTGTAATCTCAAATTTTGGATCTAAATAAAAATCCTTATAATAGAA
TACGAAGGGTGTGATTTAGCAATATGCTACACTTAAAAGAGTTGGGGATAAATAATATGCCCT
GAGCTGATTTCCATCGATAGTCTTGCTGTGGATAACCTGCCAGATTTAGAAAAATAGAAGC
TACTAACAAACCTAGATTGTCTTACATTACCCCAATGCATTTTTCAGACTCCCCAAGCTGG
AATCACTCATGCTGAACAGCAATGCTCTCAGTGCCTGTACCATGGTACCATTGAGTCTCTG
CCAAACCTCAAGGAAATCAGCATACACAGTAACCCCATCAGGTGTGACTGTGTCACTCCGTTG
GATGAACATGAACAAAAACCAACATTCGATTCATGGAGCCAGATTCAGTGTTTTGCCTGGACC
CACCTGAATTCGAAGTTCAGAATGTTCCGCAAGTGCATTTCAAGGACATGATGGAAATTTGT
CTCCCTCTTATAGCTCCTGAGAGCTTCTCTCTAATCTAAATGTAGAAGTGGGAGCTATGT
TTCCTTTCAGTGTAGAGCTACTGCAGAACCACAGCCTGAAATCTACTGGATAACACCTTCTG
GTCAAAAACCTCTTGCCCTAATACCCTGACAGACAAGTTCTATGTCCATTCTGAGGGAACACTA
GATATAAATGGCGTAACTCCAAAAGAGGGGGTTATATACTTGTATAGCAACTAACCTAGT
TGGCGCTGACTTGAAGTCTGTTATGATCAAAGTGGATGGATCTTTTCCACAAGATAACAATG
GCTCTTTGAAATATTAATAAGAGATATTTCAGGCCAATTCAGTTTGGTGTCTCGGAAGCA
AGTTTGTAAATTTCTAAATCTAGTGTTAAATGGACAGCCTTTGTCAAGACTGAAAATTTCTCA
TGCTCGCAGAAAGTCTCGAATACCATCTGATGTCAAGGTATATAATCTTACTCATCTGAATC
CATCACTGAGTATAAAATTTGTATTGATATCTCCACCATCTATCAGAAAAACAGAAAAAAA
TGTGTTAAATGTCACCACCAAAGGTTTGCAACCCTGATCAAAAAGAGTATGAAAAGAAATATAC
CACAACACTTTTGGCCCTGTCTTGGAGGCCCTTCTGGGGATTATTGGTGTGATATGCTTTATCA
GCTGCCTCTCTCCAGAAATGAACCTGTGATGGTGGACACAGCTATGTGAGGAATTTGATTCAG
AAACCAACCTTTGCAATTTAGGTGAGCTTTATCCTCCTCTGATAAATCTCTGGGAAGCAGGAAA
AGAAAAAGGTACATCACTGAAAGTAAAAGCAACTGTTATAGGTTTACCAACAAATATGTCTT
AAAAACCAAGAAACCTTCAAAAAATGAAC

FIGURE 26

MKDMPLRIHVLLGLAITTLVQAVDKKVDPCRLCTCEIRPWFTPRSIYMEASTVDCNDLGLLT
FPARLPANTQILLQLTNNIAKIEYSTDFPVNLTGLDLSQNNLSSVTNINVKMPQLLSVYLE
ENKLTTELPEKCLSELSNLQELYINHNLSTISPGAFIGLHNLRLHLNSNRLQMINSKWFDA
LPNLEILMIGENPIIRIKDMNFKPLINLRSLVIAGINLTEIPDNALVGLLENLESISFYDNRL
IKVPHVALQKVVNLFKFDLKNKPINRIRRGDFSNNMLHLKELGINNMPELISIDSLAVDNLDP
LRKIEATNNPRLSYIHPNAFFRLPKLESLMLNSNALSALYHGTTIESLPNLKEISIHNSPIRC
DCVIRWMNMNKTNIRFMEPDSLFCVDPPEFQGNVRQVHFRDMMEICPLIAPESFPSNLNV
EAGSYVSFHCRTAEPQPEIYWITPSGQKLLPNTLTDKFYVHSEGTLDINGVTPKEGGLYTC
IATNLVGADLKSVMIKVDGSFPQDNNGSLNLIKIRDIQANSVLVSWKASSKILKSSVKWTAFAV
KTENSHAAQSARIPSDVKVYNLTHLNPSTEYKICIDIPTIYQKNRKKCVNVTTKGLHPDQKE
YEKNNTTTLMACLGGLLGIIGVICLISCLSPMNCDGGHSYVRNYLQKPTFALGELYPLIN
LWEAGKEKSTSLKVKATVIGLPTNMS

Signal sequence:

amino acids 1-22

Transmembrane domain:

amino acids 633-650

N-glycosylation site.

amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,
608-612, 624-628, 625-629

Casein kinase II phosphorylation site.

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

Tyrosine kinase phosphorylation site.

amino acids 570-579

N-myristoylation site.

amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,
491-497, 492-498, 634-640, 702-708

Cell attachment sequence.

amino acids 277-280

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FIGURE 27

CCCCGGGACTGGCGCAAGGTGCCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAG
CTGCAGCCTTTTGAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTTTAC
CACGCTTGTTGGAGTAGATGAGGAATGGGCTCGTGATTATGCTGACATTCAGCAGATGAATCT
GGTAGACCTGTGGTTAACCCGTTCCCTCTCCATGTGTCTCCTCTACAAAGTTTGTCTCTTA
TGATACTGTGCTTTCATTCTGCCAGTATGTGTCCCAAGGGCTGTCTTGTCTCTCCTCTGGG
GGTTTAAATGTACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTTCTCTCTGA
AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCCAATGAAATTTTAAAG
ACCTCCATCAACTGAGAGTTCTCAACCTGTCCAAAAATGGCATTGAGTTTATCGATGAGCAT
GCCTTCAAAGGAGTAGCTGAAACCTTGCGAGACTCTGGACTTGTCCGACAATCGGATTCAAAG
TGTGCACAAAAATGCCTTCAATAACCTGAAGGCCAGGGCCAGAATTGCCAACACCCCTGGC
ACTGCGACTGTACTCTACAGCAAGTTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCCAC
AACGTGATCTGTAAACGTCCTGTTGGATGAACATGCTGGCAGACCATTCCTCAATGCTGC
CAACGACGCTGACCTTGTAACTCCCTAAAAAACTACCGATTATGCCATGCTGGTCACCA
TGTTGGCTGGTTCACTATGGTGATCTCATATGTGGTATATTATGTGAGGCAAAATCAGGAG
GATGCCCGGAGACACCTCGAATACTTGAAATCCCTGCCAAGCAGGCAGAAAGAAAGCAGATGA
ACCTGATGATATTAGCACTGTGGTATAGTGTCCAACTGACTGTCATTGAGAAAGAAAGAAA
GTAGTTTGCATTGCAGTAGAAATAAGTGGTTTACTTCTCCCATCCATTGTAAACATTTGAA
ACTTTGTATTTAGTTTTTTTTTGAATTATGCCACTGCTGAACCTTTTACAAACACTACAACA
TAAATAATTTGAGTTTAGGTGATCCACCCCTTAATTGTACCCCGATGGTATATTTCTGAGT
AAGCTACTATCTGAACATTAGTTAGATCCATCTCACTATTTAATAATGAAATTTATTTTTTT
AATTTAAAGCAAATAAAAGCTTAACCTTGAACCATGGGAAAAAAAAAAAAAAAAAAAAACA

0001033 07.304
10.12.0 33.01.0

[illegible]

Signal sequence:

Transmembrane domain:

amino acids 205-220

N-glycosylation site.

amino acids 47-51, 94-98

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 199-203

Casein kinase II phosphorylation site.

amino acids 162-166, 175-179

N-myristoylation site.

amino acids 37-43, 45-51, 110-116

FIGURE 29

ACCGAGCCGAGCGGACCGAAGGCGCGCCCGAGATG CAGGTGAGCAAGAGGATGCTGGCGGGG
GGCGTGAGGAGCATGCCAGCCCCCTCTGGCCTGCTGGCAGCCCCATCTCTGCTGGTGCT
GGGCTCAGTGCTGT CAGGCTCGGCCACGGGCTGCCCGCCGCTGGCAGTGCTCCGCCCAGG
ACCGCGCTGTGCTGTGCCACCGCAAGTGCTTTGTGGCAGTCCCCGAGGGCATCCCCACCGAG
ACGCGCCTGCTGGACCTAGGCAAGAACCGCATCAAAACGCTCAACCAGGACGAGTTCGCCAG
CTTCCCGCACCTGGAGGAGCTGGAGCTCAACGAGAACATCGTGAGCGCCGTGGAGCCCGGGCG
CCTTCAACAACCTCTTCAACCTCCGGACGCTGGGTCTCCGAGCAACCGCTGAAGCTCATC
CCGCTAGGCGCTTCTACTGGCCTCAGCAACCTGACCAAGCAGGACATCAGCGAGAACAAAGAT
CGTTATCTCTTGGACTACATGTTTTCAGGACCTGTACAACCTCAAGTCACTGGAGGTTGGCG
ACAAATGACCTCGTCTACATCTCTCACCGCGCCTTCAGCGGCCTCAACAGCTGGAGCAGCTG
ACGCTGGAGAAATGCAACCTGACCTCCATCCCCACCGAGGCGCTGTCCACCTGCACGGCCT
CATCGTCTGAGGCTCCGGCACCTCAACATCAATGCCATCCGGGACTACTCCTTCAAGAGGC
TGTACCGACTCAAGGTCTTGAGATCTCCCACTGGCCCTACTTGACACCATGACACCCAACT
TGCCTCTACGGCCTCAACCTGACGTCCCTGTCCATCACACACTGCAATCTGACCGCTGTGCC
CTACCTGGCCGTCGCCACCTAGTCTATCTCCGCTTCTCTCAACCTCTCTACAAACCCCATCA
GCACCAATTGAGGGCTCCATGTTGCATGAGCTGCTCCGGCTGCAGGAGATCCAGCTGGTGGGC
GGGCAGCTGGCCGTGGTGGAGCCCTATGCCCTTCCGCGGCCTCAACTACCTGCGCGTGCTCAA
TGTCTCTGGCAACAGCTGACCACACTGGAGGAATCAGTCTTCCACTCCGTTGGGCAACCTGG
AGACACTCATCTGGACTCCAACCCGCTGGCCTGCGACTGTCCGCTCCTGTGGGTGTTCCGG
CGCCGCTGGCGGCTCAACTTCAACCGGCAGCAGCCACGTGCGCCACGCCGAGTTTGTCCA
GGGCAAGGAGTTCAGGACTTCCCTGATGTGCTACTGCCCACTACTTCACTTCCGCGCGCG
CCCGCATCCGGGACCGCAAGGCCACGACAGGTGTTTGTGGACGAGGGCCACACGGTGCAGTTT
GTGTGCCGGGCGATGGCGACCCGCCGCCCATCTCTGGCTCTCACCCGAAAGCACTT
GGTCTCAGCCAAGACCAATGGGCGGCTCACAGTCTTCCCTGATGGCACGCTGGAGGTGCGCT
ACGCCCAGGTACAGGACAAACGGCACGTACCTGTGCATCGCGGCCAACCGCGGCGGCAACGAC
TCCATGCCCGCCCACTGCATGTGCGCAGCTACTCGCCCGACTGGCCCCATCAGCCCAACAA
GACCTTGCCTTTCATCTCCAACCGAGCGGGCGAGGGAGAGGCCAACAGCACCCGCGCCACTG
TGCTTTTCCCTTTCGACATCAAGACCTCATCATCGCCACCAACCATGGGCTTCACTCTTTT
CTGGGCGTGTCTCTTCTTGCTGGTGCTGCTGTTTCTCTGGAGCCGGGGCAAGGGCAACAC
AAAGCACAACTCGAGATCGAGATGTGCCCCGAAAGTCGGACGCAGGCATCAGCTCCGCCG
ACGCGCCCCGCAAGTTCAACATGAAGATGATATGAGGCGGGGCGGGGGCAGGGACCCCCG
GGCGGCGGGCAGGGGAAGGGCCTGGTGCACCTGCTCACTCTCCAGTCTTCCCACTC
CTCCCTACCTTCTACACAGTCTTCTTTCTCCCTCCCGCCTCCGTCCCTGCTGCCCCCCG
CCAGCCTTCAACACTGCCTCTTCTACCAGGACCTCAGAAGCCAGACCTGGGGACCCCA
CTTACACAGGGGATTGACAGACTGAGTTGAAAGCCGACGAAACCGGACGCGGCAGAGTCA
ATAATTCAATAAAAAAGTTACGAACCTTCTCTGTAACTTGGGTTTCAATAATTATGGATTTT
TATGAAACTTGAAATAATAAAAAGAGAAAAAACTAAAAAAAAAAAAAAAAAAAAA

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FIGURE 30

MQVSKRMLAGGVSRMSPSPLLACWQPILLVLVSGSVLSGSATGCPPRCECSAQDRAVLCHRKCF
VAVPEGIPTETRLDDLGNRIKTLNQDEFASFPHLEELNENIVSAVEPGAFFNNLNLRTL
GLRSNRLKLIPLGVFTGLSNLTQDISENKIVILLDYMFQDLNLSLEVGDNDLVYISHRA
FSGLNLSLEQLTLEKCNLTISIPTALSHLHGLIVLRLRHLNINAIIRDYSFKRLYRLKVLEISH
WPLYDITMTPNCLYGLNLTSLITHCNLTAVPYLAVRHLVYLRFNLNSYNPISTIEGSMLEL
LRLQETQLVGGQLAVVEPYAFRGLNLYLRLVNLVSGNQLTTLLEESVFHSGVGNLETLLILDSNPLA
CDCRLIWLWVFRRLNLFNRQQPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARIRDRKAQQV
FVDEGHTVQFVCRADGDPPPAILWLSPRKHLVSAKSNGRLTVPDGTLEVRYAQVQDNGTYL
CIAANAGGNDSPMHAHLHVRYSYSPDWP HQPNKTFAFISNQPGEGEANSTRATVPFPFDIKTLI
IATTMGFISFLGVVFLCLVLLFLWLRGKGN TKHNIEIEYVPRKSDAGISSADAPRKFNMMKI

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 556-578

N-glycosylation site.

amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345,
492-496, 505-509, 526-530, 542-546

Casein kinase II phosphorylation site.

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353,
607-611

Tyrosine kinase phosphorylation site.

amino acids 590-598

N-myristoylation site.

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143,
262-268, 320-326, 344-350, 359-365, 493-499, 503-509, 605-611

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 32-43

1021203304000

FIGURE 32

MGAPAASLLLLLLFACCWAPGGANLSQDDSQPWTSDETVVAGGTVVLKCQVKDHEDSSLQW
SNPAQQTLYFGEKRALRDNRIQLVTSTPHELISISNVALADEGEYTCSTFTMPVRTAKSLV
TVLGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGK
TFTVSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQ
KLLHCEGRGNPVPQQYLWEKEGSPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKA
YYTLNVNDPSVPSSSSTYHAIIGGIVAFIVFLLIMLIFLGHYLIRHKGTYLTHEAKGSDD
APDADTAIINAEGGQSGGDDKKEYFI

Signal sequence:

amino acids 1-20

Transmembrane domain:

amino acids 331-352

N-glycosylation site.

amino acids 25-29, 290-294

Casein kinase II phosphorylation site.

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

N-myristoylation site.

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,
306-310, 334-340, 360-364, 385-389, 386-390

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

GGGGGTAGGGAGGAAGGAATCCACCCCCACCCCCAAACCTTTTCTCTCCTTTCTCTGG
CTTCGGCAGATCGGAGCACTAAATGAATCGATTGTGTCTGTGGCGGACGAGGATGGTCGCTG
TTACTTTGTGATGAGATCGGGGATGAATTCGCTCGCTTTAAAAATCGTCTTTGGATTTGTT
GCTGGAGACGTCTCTTTGTTTTGCGCGTGGAAACGTTACAGGGGACGTTTGCAAGAGAAGA
TCTGTTTCTCGCAATGAGATAGGAAGGGGACCTACACGCTAGACGTGAAAAAAGGGCTTCACA
AGTCTGACGAGGTTTCACTAGCCCGCACTTCCGAGTTTACATTATTTCTGCAATGGCAATTC
CCTCACTCGACTCTTTCCCTAATGAGTTCGCTGAACCTTTTATAATACGGGTAGTTTGTGCAATGG
AAAAACAATGGCTTGCAATGAAAATCGTTCCGGGGGCTTTTCTGGGGCTGACGCTGTGTAAGAAG
CTGCACATCAACAACAACAGATCAAGTCTTTTCGAAAGCAGACGTTTCTGGGGCTGGACGT
TCTGGAAATATCTCCAGGCTGATTTTTAATTTATTACGAGATATAGACACCGGGGCTTCCAGG
ACTTGAACAAGCTGTGGAGGTGCTCATTTTAATAGCAATCTCACGACCGGACCTTCAAGCAAC
GTGTTCCAGTATGTGCCCATCACCACGCTGATTCGCGGAGTAAACAGGCTGAAAAACGCTGCC
CTATGAGGAGGTTCTGGAGCAAAATCCCTGGATTTCGGAGATCCTGTAGAGGATACACCTT
GGGACTCGACCTGTGATCTGCTCTCCTGGAAGAATCGGTGGAAGAACATCCCAAGAATGCC
CTGATTCGGCGGAGTGGTCTGCGAAGCGCCCCACGACGATCGAGGGTAAAGACCTCAATGAAC
CACCGAACAGGACTTGTGCTCTTTGAAAACCGAGTGGAATTAGTCTTCCGGCGGCCCTGT
CCCAAGAAGAGACCTTTGCTCCTGGACCCCTGCCAACTCCTTTCAAGACAAATGGCGAAGAG
GATCATGCGCAACACAGGGTCTGCTCCAAACGGAGGTACAAAGATCCGAGGCAACTGGCGAGT
CAAAATCAGACCCACGACGAGCAGGTACGCGGAGTGTCTCAGGAACAAACCTTAGCTAAACA
GTTTACCCTTGCCTGGGGGCTGCAGCTGCGACACATCCCAAGGCTCGGGTTTAAAGATGAAC
TGCAACAACAGGAACGTGAGCAGCTTGGCTGATTTGAAGCCCAAGCTCTCAACGTGCAGGA
GCTTTTCTACGAGATCAACAAGATCACAGCATCCGAAATCGCACTTTTGTGGATTACAAGA
ACCTCATTTCTGTTGGATCTGGGCAACAATAACATCGCTACTGTAGAGAACAACTTTCAAG
AACCTTTTGGACCTCAGGTGGCTATACATGGATAGCAATTAAGTGCACGCTGTCCGCGGAG
GAAATTCGCGGGGCTGCAAAACCTAGAGTACCTTGAACGTGGAATCAACGCTATCCAGCTCA
TCTCTCCGGGCACTTTCAATGCCATGCCAACTCAGGATCCTCATTTCAACAACAACCTGT
CTGAGGTCCCTGCTGTGGAGCTGTTGCTGGGGTCTGCTCTCTAAACTCAGGCTGCACAA
CAATTACTTCTGATACCTCCCGGTGGCAGGGGTGCTGCAGCAAGTTAACTCATCATCAGA
TAGACCTCCACGGAACCTGGGAGTGTCTCTGCACATTTGTCCTTTACGACAGTGGGCA
GAACGCTTGGGTTCCGAAGTGTGATGAGCGACCTCAAGTGTGAGACGCGCGTGAACCTCTT
TAGAAAGGATTTCAATGCTCTCTCCAATGACGAGATCTGCCCTCAGCTGTACGCTAGGATC
CGCCACGTTAACTTCGCACAGTAAAAACGACATGGGTTGGCGAGGACCGGGACGCATCC
AATCTCTACCTAGACACACGACGAGTGTCCATCTCGGTGTGTGCTCCGGGACTGCTGTGGT
GTTTGTACCTTCGCCCTTCCAGGCTGACGGGTGGGATGCTGTTTATCTGAGGAACCGAAAG
GGTCCAGAGACAGATGCCAACTCTCCGCGTCCGAGATTAAATCCCTACAGACAGTCTGT
GACTCTTCTTACGTGCCAATAGGGCTTACAAACGACATGGGGCCACAGAGTGTATAGCTG
TGECTCTCACTCGCTCTCAGACTAAGAACCAACCCCAATAGGGGAGGGGACGAGGAAGCG
ATACATCCTTCCCAACCGCAGGCACCCCGGGGCTGGAGGGCGGTGTACCAAATCCCGCGC
CCATCAGGCTGATGGGCATAAGTAGATAAATAGCTGTGAGCTGCGACCAACCGAAGGGCGC
GACCCCTTACTAGCTCCCTCTTGTAAACAAGACGAGACTGTGGAGAGCTGGGAGGCGCA
GCCAGCTCGCTCTTTGCTGAGAGCCCTTTTGACAGAAAGCCGACGACGACCTGCTGGAG
AAGTGACAGTGCCTCGCCTCGGCCCGGGGCTGTGGGTTGTGATGCGCGGCTTATAT
ATATATACATATATCCACATCTATATAGAGAGATAGATATCTATTTTTCCCTCTGTGGATTAG
CCCCGTGATGGCTCCCTGTGGCTACGACGAGGATGGGCAATGCAAGAGGATGAATGTAT
TGTAATAAGTAACCTTTGACTTCTGAC

FIGURE 34

MLLWILLLETSLCFAAGNVTDGVCKEKICSCNEIEGDLHVDCEKKGFTSLQRFTAPTSQFYH
LFLHGNSLTRLPNEFANFYNAVSLHMENNGLHEIVPGAFLGLQLVKKRLHINNKKIKSFRKQ
TFLGLDDLEYLQADFNLLRDIDPGAQDNLNKLEVLILNDNLISTLPANVFQYVPITHLDLRG
NRLKTLPIYEEVLEQIPGIAEILLEDNPWDCTCDLLSLKEWLENI PKNALIGRVVCEAPTRLQ
GKDLNETTEQDLCPLKNRVDSLLPAPPAQEETFAPGPLPTPFKTNQGEDHATPGSAPNGGTK
IPGNWQIKIRPTAAIATGSSRNKPLANSLPCPGGCSCDHI PGSGLKMNCNNRNVSSSLADLKP
KLSNVQELFLRDNKIHSIRKSHFVDYKNLILDLGNNNIATVENNTFFKNLLDLRWLYMDSNY
LDTLSREKFAGLQNLLEYLNVEYNAILQLILPGTFNAMPKLRILILNNNLLRSLPVDVFAGVSL
SKLSLHNNYFMYLFPVAGVLDQLTSIIQIDLHGNPWECSCCTIVPFKQWAERLGSSEVLMSDLKC
ETPVNFFRKDFMLLSNDEICPQLYARISPTLTSHSKNSTGLAETGTHSNSYLDTSRVSISVL
VPGLLLVFVTSFTVVGMLVFILRNKRKSKRRDANSSASEINSLQTVCDSSYWHNGPYNADG
AHRVYDCGSHSLSD

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 618-638

N-glycosylation site.

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 122-126, 646-650

Casein kinase II phosphorylation site.

amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577,
608-612, 657-661, 666-670, 693-697

N-myristoylation site.

amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,
354-360, 465-471, 493-499, 598-604, 603-609

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 337-348

FIGURE 35

AGTCGACTGCGTCCCCTGTACCCGGCGCCAGCTGTGTTCCTGACCCAGAACTAACTCAGGGC
TGCACCGGGCCCTGGCAGCGCTCCGACACATTTCTCTGTCGCGGCCCTAAGGGAAACTGTTGGC
CGCTGGGCCCGCGGGGGATTCTTGGCAGTTGGGGGGTCCGTCCGGAGCGAGGGCGGAGGGG
AAGGGAGGGGGAACCGGTTGGGGAAGCCAGCTGTAGAGGGCGGTGACCGCGCTCCAGACAC
AGCTCTGCGTCTCTGAGCGGGACAGATCCAAGTTGGGAGCAGCTCTGCGTGCGGGGCTCAG
AGAATGAGGCGCGCGTTTCGCCCTGTGCCCTCCTCTGGCAGGCGCTCTGGCCCCGGGCGGGCGG
CGGCCAACACCCCACTGCCAGCCGTGCTGGCTGCTCGGCCCTCGGGGGCTGCTACAGCCTCG
ACCAGCTACCATGAAGCGGCAGGCGGCCGAGGAGGCTGCATCCTGCGAGGTGGGGCGCTC
AGCACCGTGGCTGCGGGCGCCGAGCTGCGCGCTGTGCTCGCGCTCCTGCGGGCAGGCCCCAGG
GCCCGAGGGGGCTCCAAGACCTGCTGTTCTGGGTGCGACTGGAGCGCAGGCGTTCCTCACT
GCACCTTGGAGAACGAGCCTTTGCGGGGTTTCTCCTGGCTGTCTCCGACCCCGCGGTCTC
GAAAGCGACACGCTGCAGTGGGTGGAGGAGCCCCAACGCTCCTGCACCGCGCGAGATGCGC
GGTACTCCAGGCCACCGGTGGGGTGCAGCCCCGAGGCTGGAAGGAGATGCGATGCCACCTGC
GCGCCAACGGCTACCTGTGCAAGTACCAAGTTTGAGGTCTTGTGTCTGCGCCGCGCCCCGGG
GCGCGCTCTAACTTGAGCTATCGCGCGCCCTTCAGCTGCACAGCGCCGCTCTGGACTTCAG
TCCACCTGGGACCGAGGTGAGTGCCTCTGCGGGGACAGCTCCCGATCTCAGTTACTTTGCA
TCGCGGACGAAATCGGCGCTCGCTGGGACAACTCTCGGGCGATGTGTTGTGTCCCTGCCCC
GGGAGGTACCTCCGTGCTGGCAAAATGCGCAGAGCTCCCTAAGTGCCTAGACGACTTTGGGAGG
CTTTGCCCTGCGAATGTGCTACGGGCTTCGAGCTGGGGAAGGACGGCCGCTCTTGTGTGACCA
GTGGGGAAGGACAGCCGACCTTGGGGGACCGGGGTGCCACAGGCGCCCCCGGCCACT
GCAACCAGCCCCGTGCCGACAGAAACATGGCCAATCAGGGTCGACGAGAAGCTGGGAGAGAC
ACCACTTGTCCCTGAAACAAGACAATTACAGTAACATCTATTCTGAGATTCTCGATGGGGAT
CACAGAGCAGATGTCTACCTTCAAATGTCCCTTCAAGCCGAGTCAAAGGCCACTATCACC
CCATCAGGGAGCGTGATTTCCAAGTTAATTCTACGACTTCTCTGCCACTCCTCAGGCTTT
CGACTCCTCCTCTGCGCGTGGTCTTCAATTTGTGAGCAGCAGTAGTAGTGTGGTGATCT
TGACCATGACAGTACTGGGGCTTGTCAAGCTCTGCTTTCACGAAAGCCCTCTTCCAGCCA
AGGAAGGAGTCTATGGGCCCGCCGGGCTTGGAGAGTGATCCTGAGCCCGCTGCTTTGGGGCTC
CAGTTCTGCACATTGCACAAACAAATGGGGTGAAAGTCGGGGACTGTGATCTGCGGGACAGAG
CAGAGGGTGCTTTGCTGGCGGAGTCCCTCTTGCTCTAGTGATGCATAGGGGAAACAGGGGA
CATGGGCACCTCTGTGAACAGTTTTTCACTTTTGATGAAACGGGGAAACAGAGGAACCTTAC
TTGTGTAAC TGACAATTTCTGCAGAAATCCCCCTTCTCTAAATTTCCCTTTACTCCACTGAG
GAGCTAAATCAGAACTGCACACTCCTTCCCTGATGATAGAGGAAGTGGAAGTGCCTTTAGGA
TGGTGATATCGGGGACCGGGTAGTGCTGGGGAGAGATATTTCTTATGTTTATTCGGAGAA
TTTGAGAGAAGTGATGAACTTTTCAAGACATTGAAACAAATAGAACACATATAATTTACA
TTAAAAAATAATTTCTACAAAAATGGAAGGAAATGTTCTAGTTGTCAGGCTAGGAGTAT
ATTGGTTCCGAAATCCCGGGGAAAAAATAAAAAATAAAATTAAGGATTGTGTAT

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TOGETHER

FIGURE 36

MRPAFALCLLWQALWPGPGGGGEHPTADRAGCSASGACYSLHHATMKRQAAEEACILRGGALS
TVRAGAE LRAVLALLRAGPGPGGSKDLLFWVALERRRSHCTLENEPLRGFSWLSSDPGGLE
SDTLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLCPAFRPGA
ASNLGYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCIADBEIGARWDKLSGDVLCPCPG
RYLRAGKCAELPNCDDLLGGFACECATGFELGKDGRCVTS GEGQPTLGGTGVPTRRPPATA
TSPVPQRTWPIRVDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQMSLQAESKATITP
SGSVISKFNSTTSSATPQAFDSSSAVVFI FVSTAVVVLVILTMTVLGLVKLCFHESPSSQPR
KESMGPPGLESDPEPAALGSSSAHCTNNGVKVGDCDLRDRAEGALLAESPLGSSDA

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 189-193, 381-385

Glycosaminoglycan attachment site.

amino acids 289-293

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 98-102, 434-438

Casein kinase II phosphorylation site.

amino acids 275-279, 288-292, 342-346, 445-449

N-myristoylation site.

amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,
477-483

Aspartic acid and asparagine hydroxylation site.

amino acids 262-274

FIGURE 37

CGGACGCGTGGGATTACAGCAGTGGCCTGTGGCTGCCAGAGCAGCTCCTCAGGGGAACTAAG
CGTCGAGTCAGACGGCACCATAATCGCCTTTAAAGTGCCTCCGCCCTGCCGCCCGGTATC
CCCCGGCTACCTGGCCCGCCCGCGCGGTGCGCGCGTGAGAGGGAGCGCGCGGGCAGCCGA
GCGCCGGTGTGAGCCAGCGCTGCTGCCAGTGTGAGCGGCGGTGTGAGCGCGGTGGGTGCGGA
GGGGCGTGTGTGCCGCCGCGCGCCGTGGGGTGCAAAACCCGAGCGCTACGCTGCCATGA
GGGGCGCGAAACGCTGGGGCGCCACTCTGCCTGTGCTGGCTGCCGCCACCCAGCTCTCGCGG
CAGCAGTCCCCAGAGAGACCTGTTTTACATGTGGTGGCATTCTTACTGGAGAGTCTGGGATT
TATTGGCAGTGAAGGTTTTCTGGAGTGTACCTCCAAATAGCAAATGTACTTGGAAAATCA
CAGTTCCCCGAAGAAAAGTAGTCGTTCTCAATTTCCGATTCTAGACCTCGAGAGTGACAAC
CTGTGCCGCTATGACTTTGTGGATGTGTACAATGGCCATGCCAATGGCCAGCGCATTGGCCG
CTTCTGTGGCACTTCCGGCCTGGAGCCCTTGTGTCCAGTGGCAACAAGATGATGGTGCAGA
TGATTTCTGATGCCAACACAGCTGGCAATGGCTTCATGGCCATGTTCTCCGCTGCTGAACCA
AACGAAAGAGGGGATCAGTATTGTGGAGGACTCCTTGACAGACCTTCGGCTCTTTTAAAC
CCCCAACTGGCCAGACCGGGATTACCTGCGAGGAGTCACTTGTGTGGCACATTGTAGCCC
CAAAGAATCAGCTTATAGAATTAAAGTTTGAGAGTTTGATGTGGAGCGAGATAACTACTGC
CGATATGATTATGTGGCTGTGTTTAAATGGCGGGGAAGTCAACGATGCTAGAAGAATTGGAAA
GTATTGTGTGATAGTCCACCTGCGCCAATTGTGTCTGAGAGAAAATGAACCTTCTATTTCAGT
TTTTATCAGACTTAAGTTTAACTGCAGATGGGTTTATTGGTCACTACATATTCAGGCCAAAA
AAACTGCCTACAACCTACAGAACAGCCTGTCACCACCACATTCCCTGTAACCAACGGGTTTAAA
ACCCACCGTGGCCCTGTGTCAACAAAAGTGTAGACGGACGGGGACTCTGGAGGGCAATTATT
GTTCAAGTGACTTTGTATTAGCCGGCACTGTTATCACAACCATCACTCGCGATGGGAGTTTG
CAGCCACAGTCTCGATCATCAACATCTACAAAGAGGGAAATTTGGCGATTACGACGGCGGG
CAAGAACATGAGTGCCAGGCTGACTGTGCTCTGCAAGCAGTGCCCTCTCCTCAGAAGAGGTC
TAAATTACATTATTATGGGCCAAGTAGGTGAAGATGGGCGAGGCCAAAATCATGCCAAACAGC
TTTATCATGATGTTCAAGACCAAGAAATCAGAAGCTCCTGGATGCCTTAAAAAATAAGCAATG
TTAAAGTGAACCTGTGTCCATTTAAGCTGTATTCTGCCATTGCCTTTGAAAGATCTATGTTT
TCTCAGTAGAAAAAAAATACTTATAAAATTAACATATTCTGAAAGAGGATTCGAAAAGATGG
GACTGGTTGACTCTTACATGATGGAGGTATGAGGCCCTCCGAGATAGCTGAGGGAAAGTTCTT
TGCCCTGCTGTGAGAGGACGCTATCTGATTGGAACCTGCCGACTTAGTGCGCGGTGATAGGA
AGCTAAAAGTGTCAAGCGTTGACAGCTTGAAGCGTTTATTTATACATCTCTGTAAAAGGAT
ATTTTAGAATTGAGTTGTGTGAAGATGTCAAAAAAGATTTTAGAAGTGCAATATTATAGT
GTTATTGTTTCACTTCAAGCCCTTGCCCTGAGGTGTTACAATCTGTGCTGCGTTTCTA
AATCAATGCTTAATAAAATATTTTTAAAGGAAAAA

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FIGURE 38

MRGANAWAPLCLLLAAATQLSRQQSPERPVTTCGGILTGESGFIGSEGFPGVYPNSKCTWK
ITVPEGKVVLNFRFIDLESNLCRYDFVDVYNHANGQRIGRFCGTFRPGALVSSGNKMMV
QMISDANTAGNGFMAMFSAAEPNERGDQYCGLLDRPSGSFKTPNWPDRDYPAGVTCVWHIV
APKNQLIELKFEKFDVERDNYCRYDYVAVFNGGEVNDARRIGKYCGDSPAPPIVSEARNELLI
QFLSLSLTADGFIGHYIFRPKKLPPTTEQPVTTTFFPVTTGLKPTVALCQQKCRRTGTLEGN
YCSSFVLAGTVITTITRDGSLHATVSIINIYKEGNLAIQQAGKNMSARLTVVCKQCPLLR
GLNYIIMGQVGEDGRGKIMPNSFIMMFKTNQKLLDALKNKQC

Signal sequence:

amino acids 1-23

N-glycosylation site.

amino acids 355-359

Casein kinase II phosphorylation site.

amino acids 64-68, 142-146, 274-278

Tyrosine kinase phosphorylation site.

amino acids 199-208

N-myristoylation site.

amino acids 34-40, 35-41, 100-106, 113-119, 218-224, 289-295,
305-311, 309-315, 320-326, 330-336

Cell attachment sequence.

amino acids 149-152

FIGURE 39

CGGACGCGTGGGCGGACGCGTGGGCGGCCACGGCGCCCGCGGGCTGGGGCGGTGCGTTCTT
CCTTCTCCGTGGCTACGAGGGTCCCCAGCCTGGGTAAAGATGCCCCCATGGCCCCGAAGG
GCCTAGTCCCAGCTGTGCTCTGGGGCCTCAGCCTCTTCTCAACCTCCCAGGACCTATCTGG
CTCCAGCCCTCTCCACCTCCCCAGTCTTCTCCCCGCCTCAGCCCCATCCGTGTCATACCTG
CCGGGGACTGGTTGACAGCTTTAACAGGGCCTGGAGAGAACCATCCGGGACAACTTTTGAG
GTGGAACACTGCCTGGGAGGAAGAGAATTGTCCAATACAAAGACAGTGAGACCCGCCTG
GTAGAGGTGCTGGAGGGTGTGTGCAGCAAGTCAGACTTCGAGTGCCACCGCCTGCTGGAGCT
GAGTGAGGAGCTGGTGAGAGCTGGTGGTTTCAACAGCAGCAGGAGGCCCGGACCTCTTCC
AGTGCTGTGCTCAGATTCCCTGAAGCTCTGTGCCCCGACGGCACCTTCGGGGCCTCCTGC
CTTCCCTGTCTGGGGGAACAGAGAGGCCCTGCGGTGGCTACGGGCAGTGTGAAGGAGAAGG
GACACGAGGGGGCAGCGGGCACTGTGACTGCCAAGCCGGCTACGGGGGTGAGGCCTGTGGCC
AGTGTGGCCTTGGCTACTTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTTTCGGCTTGT
TTTGGCCCCCTGTGCCGATGCTCAGGACCTGAGGAATCAAACCTGTTGCAATGCAAGAAGGG
CTGGGCCCTGCATCACCTCAAAGTGTGTAGACATTGATGAGTGTGGCACAGAGGGAGCCAAC
GTGGAGCTGACCAATTCTGCGTGAACACTGAGGGCTCCTATGAGTGCCGAGACTGTGCCAAG
GCCTGCCTAGGCTGCATGGGGGACGGGCCAGGTGCTGTAAGAAGTGTAGCCCTGGCTATCA
GCAGGTGGGCTCCAAGTGTCTCGATGTGGATGAGTGTGAGACAGAGGTGTGTCCGGGAGAGA
ACAAGCAGTGTGAAAAACCGAGGGCGGTTATCGCTGCATCTGTGCCGAGGGCTACAAGCAG
ATGGAAGGCATCTGTGTGAAGGAGCAGATCCAGAGTCAGCAGGCTTCTTCTCAGAGATGAC
AGAAGACGAGTTGGTGGTGTGCTGCAGCAGATGTTCTTTGGCATCATCATCTGTGCACTGGCCA
CGCTGGCTGCTAAGGGCGACTTGGTGTTCACCGCCATCTTCATTGGGGCTGTGGCGGCCATG
ACTGGCTACTGGTTGTCTAGAGCGCAGTGACCGTGTGCTGGAGGGCTTCATCAAGGGCAGATA
ATCGCGGCCACCACCTGTAGGACCTCCTCCACCCACGCTGCCCCAGAGCTTGGGCTGCCC
TCCTGTCTGGACACTCAGGACAGCTTGGTTTATTTTGGAGAGTGGGGTAAGCACCCCTACCTG
CCTTACAGAGCAGCCCAGGTACCCAGGCCCGGGCAGACAAGGCCCTCGGGTAAAAAGTAGC
CCTGAAGGTGGATACCATGAGCTCTTCACTGGCGGGGACTGGCAGGCTTCACAATGTGTGA
ATTTCAAAGTTTCTTCTTAATGGTGGCTGCTAGAGCTTTGGCCCTGCTTAGGATTAGGTG
GTCTCTACAGGGGTGGGGCCATCACAGCTCCCTCCTGCCAGTCGATGCTGCCAGTTCTCTGT
TCTGTGTTCAACCATCCCCACACCCCATTGCCACTTATTTATCTCATCTCAGGAATAAAGA
AAGGTCTTGAAAGTTAAAAA

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FIGURE 40

MAPWPPKGLVPAVLWGLSLFLNLP GPIWLQPSPPQSSPPPPQHPCHTCRGLVDSFNKGLER
TIRDNFGGGNTAWEENLSKYKDSETRLVEVLEGVCSKSDFECHRLLLELSEELVESWWFHKQ
QEAPDLFQWLCSDSLKLCPPAGTFGPSCLPCPGGTERPCGGYGQCEGEGTRGSGHCDQAG
YGGACGQCGLGYFEAERNASHLVCSACFGPCARCSGPPEESNCLQCKKGWALHHLKCVDIDE
CGTEGANCGADQFCVNTGSEYECRDCAKACLGCMGAGPGRCKKCSPGYQQVGSKCLDVDECE
TEVCPGENKQCENTEGGYRCICAEGYKQMEGICVKEQIPESAGFFSEMTEDELVVLLQQMFPG
IIICALATLAAKGLDVFTAIPTFGAVAAMTGYWLSERSDRVLEGFIKGR

Signal sequence:

amino acids 1-29

Transmembrane domain:

amino acids 372-395

N-glycosylation site.

amino acids 79-83, 205-209

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 290-294

Casein kinase II phosphorylation site.

amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-263

N-myristoylation site.

amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173, 173-179,
177-183, 188-194, 250-256, 253-259, 267-273, 280-286, 283-289,
326-332, 372-378, 395-401

Aspartic acid and asparagine hydroxylation site.

amino acids 321-333

EGF-like domain cysteine pattern signature.

amino acids 181-193

00000000

TTGAGACCCCTCTGTCAGCCTTCTCAAGGGACAGCCCCACTCTGCCTCTTGCTCTCCAGGGCA
GCACCATGCAGCCCTGTGGCTCTGCTGGGCACTCTGGGTGTTGCCCTTGGCCAGCCCCGGG
GCCGCCCTGACCGGGGAGCAGCTCCTGGGCAGCCTGCTGCGGCAGCTGCAGCTCAAGAGGT
GCCACCCCTGGACAGGGCCGACATGAGGAGCTGGTCATCCCCACCCACGTGAGGGCCAGT
ACGTGGCCCTGCTGTCAGCGCAGCCACGGGGACCGTCTCCGCGGAAAGAGGTTTCAGCCAGAGC
TTCCGAGAGGTTGGCCGCGAGGTTCTTGGCGTTGGAGGCCAGCACACCTGCTGGTGTTGCG
CATGGAGCAGCGGCTGCCGCCAACAGCGAGCTGGTGCAGGCCGTGCTGCGGCTCTTCCAGG
AGCCGGTCCCCAAGGCCGCGCTGCACAGGCACGGGCGGTGTCCCCGCGCAGCGCCCGGGCC
CGGGTGACCGTCGAGTGGCTGCGCGTCCGCGACGACGGCTCCAACCGCACCTCCCTCATCGA
CTCCAGGCTGGTGTTCCGTCCACGAGAGCGGCTGGAAGGCCTTCGACGTGACCGAGGCCGTGA
ACTTCTGGCAGCAGCTGAGCCGGCCCCGCGACCGCTGCTGCTCAAGGTGTCCGTGCAGAGG
GAGCATCTGGGGCCCGTGGCGCTCCGCGCCCCACAAGCTAGCTCCGCTTTCCTTCGACGGGCG
GCCAGCCGGGCTTTGGGAGCCCCAGCTGGAGCTGCACACCTTGACACTTGGGGACATATGAG
CTCAGGGCGACTGTGACCCTGAAGCACCAATGACCGAGGGCACCCGCTGCTGCGGCCAGGAG
ATGTACATTGACCTGCAGGGGATGAAGTGGGCGGAGAACTGGGTGCTGGAGCCCCGGGCTT
CCTGGCTTATGAGTGTGTGGGCACCTGCCGCGAGCCCCCGGAGGCCCTGGCCTTCAAGTGGC
CGTTTCTGGGGCTTCGACAGTGCATCGCCTCGGAGACTGACTCGCTGCCATGATCGTCAGC
ATCAAGGAGGGAGGCAGGACCAGGCCCAAGTGGTCAGCCTGCCAACATGAGGGTGCGAGAA
GTGCAGCTGTGCTCGGATGTTGCGCTCTGCCAAGGAGGCTCCAGCCATTAGGCGCCTAGTG
TAGCCATCGAGGGACTTGACTTGTGTGTGTTTCTGAAGTGTTCGAGGGTACCAGGAGAGCTG
GCGATGACTGAACTGCTGATGGACAAATGCTCTGTGCTCTCTAGTGAGCCCTGAATTGTCTT
CCTCTGACAAGTTACCTCACCTAATTTTTGCTTCTCAGGAATGAGAACTTTTGGCCACTGGA
GAGCCCTTGCTCAGTTTTCTCTATTCTATTATTCACTGCATATATTCTAAGCACTTACAT
GTGGAGATACTGTAACCTGAGGGCAGAAAGCCANTGTGTCAATTGTTTACTTGTCTGTCTAC
TGGTCTCGGGCTAAAGTCCTCCACCACCACTCTGGACCTAAGACCTGGGGTTAAGTGTGGGT
TGTGATCCCCAATCCAGATAATAAAGACTTTGTA~~AA~~ACATGAATA~~AA~~ACACATTTTATTCT
~~AA~~AA

FIGURE 42

MQPLWLCWALWVLPPLASPGAALTGEQLLGSLLRQLQLKEVPTLDRADMEELVIPTHVRAQYV
ALLQRSHGDRSRGKRFSQSFRVAGRFLALEASTHLLVFGMEQRLPPNSELVQAVLRLFQEP
VPKAALHRHGRLSPRSARARVTVEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDVTBAVNF
WQQLSRPRQPLLLQVSVQREHLGPLASGAHKLVRFASQGAPAGLGEPQLELHTLDDLGDYGAQ
GDGCDPEAPMTBETRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCCRQPPEALAFKWPF
LGPRQCIASETDSLPMIVSIKEGGRTRPQVVSLENMRVQKCSASCSDGALVPRRLQP

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 158-162

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 76-80

Casein kinase II phosphorylation site.

amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

N-myristoylation site.

amino acids 19-25, 156-162, 225-231, 260-266, 274-280

Amidation site.

amino acids 74-78

TGF-beta family signature.

amino acids 282-298

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ECTCTGTTCCCAAGGAGTCCCTTCGGCGGCTGTTGTGTCACTGGCCTGATCGCGAATGGGGACAAAG
 GGCGCAAGTCGAGAGGAAACTGTTGTGCCTCTTCATATTTGGCGATCCTGTTGTGCTCCCTGG
 CATTTGGGCAGTGTTACAGTGCACCTCTCTGAACCTGAAGTCAGAATTCCTGAGAATAATCCT
 GTGAAGTTGTCTGTGCCTACTCGGGCTTTTCTTCTCCCCGTGTGGAGTGAAGTTTGACCA
 AGGAGACACCACCAGACTCGTTTGCTATAATAACAAGATCACAGCTTCCTATGAGGACCGGG
 TGACCTTCTTGCCAACTGGTATCACCTTCAAGTCCGTGACACGGGAAGACACTGGGACATAC
 ACTTGTATGGTCTCTGAGGAAGGCGGCAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGT
 GCTTGTGCCTCCATCCAAGCCTACAGTTAAACATCCCCCTCTCTGCCACCATTGGGAACCGGG
 CAGTGTGACATGCTCAGAACAAGATGGTTCCCCACCTTCTGAATACACCTGGTTCAAAGAT
 GGGATAGTGTATGCCTACGAATCCCAAAGCACCCGTGCCTTCAGCAACTCTTCTATGTCTCT
 GAATCCCACAACAGGAGAGACTGGTCTTTGATCCCCCTGTCAGCTCTGATACGTGAGAATA
 CAGTGTGAGGCACGGAATGGTATGGGACACCCACTGACTTCAAATGTGTGCGCATGGAAGCT
 GTGGAGCGGAATTGGGGGTTCATCGTGGCAGCCCTCTTTGAACCTGATTTCTCTGGGAAT
 CTTGGTTTTTGGCATCTGGTTTGCTATAGCCGAGGCCACTTTGACAGAACAAAGAAAGGGA
 CTTGAGTAAGAAGGTGATTTACAGCCAGCCTAGTGCCGGAAGTGAAGGAGAATTCAAACAG
 ACCTCGTCATTCTGTGTTGAGCCCTGGTTCGGCTCACCGCCTATCATCTGCATTTGCCCTTACT
 CAGGTGCTACCGGACTCTGGCCCCGTATGCTGTAGTTTACAGGATGCCTTATTTGTCTTC
 TACACCCACAGGGCCCCCTACTTCTTCGGATGTGTTTTTAATAATGTCAGCTATGTGCCCC
 ATCCTCCTTCATGCCCTCCCTCCCTTTCTTACCCTGCTGAGTGGCTGGAACTTGTTTTAA
 GTGTTTATTCCCATTCTTTTGGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCC
 TTTCTAAGTAGACAGCAAAAAATGGCGGGGTTCGAGGAATCTGCACCTCAACTGCCACCTGGC
 TGGCAGGGATCTTTGAATAGGTATCTTGAGCTTGTTCTGGGCTCTTTCTCTGTGTACTGAC
 GACCAGGGCCAGCTGTTCTAGAGCGGGAATTAGAGGCTAGAGCGGCTGAATGTTGTTTGG
 TGATGACACTGGGGTCTCTCCATCTCTGGGGCCCACTCTCTTCTGTCTTCCCATGGGAAGTG
 CCACTGGGATCCTCTGCCCCGTCTCTTGAATACAAGCTGACTGACATTGACTGTGTCTGT
 GGAAAATGGGAGCTCTTGTTGTGGAGAGCATAGTAAATTTTCAGAGAACTTGAAGCCAAAG
 GATTTAAAAACCGCTGCTCTAAAGAAAAAGAACTGGAGGCTGGGCGCAGTGGCTCACGCCCT
 TAATCCGAGAGGCTGAGGCAGGCGGATCACTTGAGGTCGGGATCTCGGATCAGCTCGCTGACCA
 CATCTGGAGAAACCTACTGGAATAACAAAGTTAGCCAGGCATGGTGTGTCATGCTGTAGTCT
 CCAGCTGCTCAGGAGCTTGCCAAACAAGAGCAAACTCCAGCTCAAAAAA

Figure 1. Schematic diagram of the experimental setup. The subject is seated in a chair and views the target through a video camera. The target is a vertical rod with a horizontal bar at the end. The subject's hand is positioned at the end of the bar. The distance between the subject's hand and the target is 100 cm. The target is 10 cm in diameter. The subject's hand is 10 cm in diameter. The subject's hand is 10 cm in diameter. The subject's hand is 10 cm in diameter.

Signal sequence:

Transmembrane domain:

N-glycosylation site.

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 270-274

Casein kinase II phosphorylation site.

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,
193-197, 203-207, 287-291

N-myristoylation site.

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

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CACGCGCTGGCCGGCCCGCTGTGGGGACAGCATGAGCGCGGTTGGATGGCGCAGGTTGGA
GCGTGGCGAACAGGGGCTCTGGGCCTGGCGCTGCTGCTGCTCGGCCCTCGGACTAGGCCT
GGAGGCGCGCCGAGCCCGCTTTCACCCCGACCTCTGCCAGGCCGAGGCCCCAGCTCAG
GCTCGTGCCACCCACCAAGTTCAGTGCCGACCAAGTGGCTTATGCGTGCCCTTCACTTG
CGCTGCGACAGGGACTTGGACTGCAGCGATGGCAGCGATGAGGAGGAGTGCAGGATTGAGCC
ATGTATCCCAGAAAGGGCAATGCCACCGCCCCCTGGCCTCCCTGCCCTGCACCGGCGTCA
GTGACTGCTCTGGGGAACTGACAAGAACTGCGCAACTGCACCGCCTGGCCTGCCTAGCA
GGCAGCTCCGTTGTACAGCTGAGCAGTACTGCTCATTCCACTCAGCTGGCGCTGCGACGGCCA
CCCAGACTGTTCCGACTCTCAGCAGCAGTCTCGGCTGTGGAAACCAATGAGATCTCCCGGAAG
GGGATGCCACAACCATGGGGCCCCCTGTGACCCTGGAGAGTGTCCCTCTGTGCGGAATGCCACATCTC
ACAACCATGGGGCCCCCTGTGACCCTGGAGAGTGTCCCTCTGTGCGGAATGCCACATCTC
CTCTGCCGGAGACCAGTCTGGAAGCCCAACTGCCTATGGGGTTATTGACAGTGTCTGCGGTGC
TCAGTGCAAGCCTGGTCAACGCCACCCTCCTCCTTTTGTCTGGCTCCGAGCCAGGAGCGC
CTCGCCCACTGGGGTTACTGGTGCCATGAAGGAGTCCCTGCTGCTGTGAGAACAGAAGAC
CTCGCTGCCCTGAGGACAAGCACTTGCCACCACCGTCACTCAGCCCTGGGGCTAGCCGGACA
GGAGGAGAGCAGTGATGCGGATGGGTACCCGGGCACACCAGCCCTCAGAGACCTGAGTTCTT
CTGGCCACGTGGAACCTCGAACCCGAGTCTCTGCAGAAGTGGCCCTGGAGATTGAGGGTCCC
TGGACACTCCCTATGGAGATCCGGGGAGCTAGGATGGGGAACCTGCCACAGCCAGAACTGAG
GCGCTGGCCCCAGGCAGCTCCCAAGGGGTAGAACGGCCCTGTGCTTAAGACACTCCCTGCTG
CCCCGTCTGAGGGTGGCGATTAAAGTTGCTTC

FIGURE 46

MSGGWMAQVGAWRTGALGLALLLLLLLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCR
TSGLCVPLTWRCRDLDCSDGSDEEECRIEPTQKGQCPPPPGLPCPCTGVSDCSGGTDKKL
RNC SRLACLAGE LRCTLSDDCIPLTWRC DGH PDCPDSSDELGC GTNEILPEG DATTMGP PVT
LESV TSLRNATTMGPPV TLESVPSVGNATSSSAGDQSGSPTAYGVIAAAVLSASLV TATLL
LLSWLRAQERLRPLGLLVAMKESLLLSEQKTSLP

Signal sequence:

amino acids 1-30

Transmembrane domain:

amino acids 230-246

N-glycosylation site.

amino acids 126-130, 195-199, 213-217

Casein kinase II phosphorylation site.

amino acids 84-88, 140-144, 161-165, 218-222

N-myristoylation site.

amino acids 3-9, 10-16, 26-32, 30-36, 112-118, 166-172, 212-218,
224-230, 230-236, 263-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 44-55

Leucine zipper pattern.

amino acids 17-39

0713101

CCACACGCGTCGGGTCTCGCTCGCTCGCGCAGCGGCGGCAGCAGAGGTCGCGCACAGATGCGG
GTTAGACTGGCGGGGGGAGGAGGCGGAGGAGGGAAGGAAGCTGCATGCATGAGACCCACAGA
CTCTTGCAAGCTGGATGCCCTCTGTGGATGAAAGATGTATCATGGAATGAACCCGAGCAATG
GAGATGGATTCTAGAGCAGCAGCAGCAGCAGCAGCAACCTCAGTCCCCCAGAGACTCTTG
GCCGTGATCCTGTGGTTTCAGCTGGCGCTGTGCTTCGGCCCTGCACAGCTCACGGGCGGGTT
CGATGACCTTCAAGTGTGTGCTGACCCCGGCATTCCCGAGAATGGCTTCAGGACCCCCAGCG
GAGGGGTTTCTTTGAAGGCTCTGTAGACCCGATTTCAGTCCCAAGACGGATTCAAGCTGAAG
GGCGCTACAAAGAGACTGTGTTTGAAGCATTTTAAATGGAACCTTAGGCTGGATCCCAAGTGA
TAATTCATCTGTGTGAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTCATA
ACAAGACATATAGACATGGAGAGAAGCTAATCATCACTTGTGCATGAAGGATTCAAGATCCGG
TACCCCGACCTACACAATATGGTTTCATTATGTGCGGATGATGGAACGTGGAATAATCTGCC
CATCTGTCAAGGCTGCCCTGAGACCTCAGCCTCTCTCTAATGGCTATGTAAACCATCTGTAGC
TCCAGACCTCCTTCCCGGTGGGGAGTGTGATCTCTCATGTGCTATTCCCGGATTTAAACTT
GATGGGTCTCGGTATCTTGAGTGCTTACAAAACTTATCTGGTCTGTCAGGCCACCCCGGTG
CCTTGCTCTGGAAGCCCAAGTCTGTCCACTACCTCCAATGGTGAGTCACGGAGATTTCGTCT
GCCACC CGCGCCTTGAGCGCTACAACCACGGAACTGTGGTGGAGTTTACTGCGATCCT
GGCTACAGCCTCACCAGCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTTCTTTC
TTATCAAGTCTACTGCATCAAATCAGAGCAAACTGGGCCCAGACCCATGAGACCTCCTGA
CCCGTGGAAGATTGTGGCGTTACCGGCAACCAGTGTGCTGCTGGTGCTGCTGCTCGTCATC
CTGGCCAGGATGTTCAGACCAAGTTCAAGGCCCACTTTCCCCCAGGGGGCCTCCCGGAG
TTCAGCAGTGAACCTGACTTTGTGGTGGTAGACGGCGTGCCCGTCATGCTCCCGTCTCTATG
ACGAAGCTGTGAGTGGCGGCTTGAGTGCCCTAGGCCCCGGGTACATGGCCTCTGTGGGCCAG
GGCTGCCCCCTTACCCGTGGACGACGAGACCCCCAGCATACCCCGGCTCAGGGGACACGGA
CACAGGCCCAGGGGAGTCAGAAAACCTGTGACAGCGTCTCAGGCTCTTCTGAGCTGCTCCAAA
GTCTGTATTACCTCCAGGTGCCAAGAGAGCACCCACCCTGCTTCGGACAAACCTGACATA
ATTGCCAGCACGGCAGAGGAGGTGGCATCCACGATCCCGAGGCATCCATCATGCCCACTGGGT
GTTGTTCTAAGAAACTGATTGATTAATAAAATTTCCCAAAGTGTCCTGAAGTGTCTCTTCAA
ATACATGTTGATGTGTGGAGTGTGATCTCTTCTCTCTCTTGTTTATAGCAAAATGTAAACAA
AGCTCTGATCCTTTAAATTGCTATGCTGATAGAGTGGTGAGGCGTGAAGCTTGATCAAGTC
CTGTTTCTTCTTGACACAGACTGATTAATAAAATTTAAAGNAAAAAA

FIGURE 49

CCCACGCGTCCGCTCCGCGCCCTCCCCCGCCTCCCGTGCGGTCCGTCCGTGGCCCTAGAGA
TGCTGCTGCCGCGGTTGCAGTTGTGCGGCACGCCTCTGCCCGCAGCCCGCTCCACCGCCGT
AGCGCCCGAGTGTGCGGGGGCGCACCCGAGTCCGGCCATGAGGCCGGGAACCGCGCTACAGG
CCGTGCTGCTGGCCGTGCTGCTGGTGGGCTGCGGGCCGCGACGGGTGCGCTGCTGAGTGCC
TCGGATTTGGACCTCAGAGGAGGGCAGCCAGTCTGCCGGGAGGGACACAGAGGCCTTGTTA
TAAAGTCATTTACTTCCATGATACTTCTCGAAGACTGAACTTTGAGGAAGCCAAAGAAGCCT
GCAGAGGGGATGAGAGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAAACTGATAGAA
AAGTTCATTGAAAACCTCTTGCCATCTGATGGTGACTTCTGGATTGGGCTCAGGAGGCGTGA
GGAGAAACAAAGCAATAGCACAGCCTGCCAGGACCTTTATGCTTGGACTGATGGCAGCATAT
CACAATTTAGGAACTGGTATGTGGATGAGCCGTCCTGCCGCAGCGAGGTCTGCGTGGTCATG
TACCATCAGCCATCGGCACCCGCTGGCATCGGAGGCCCTACATGTTCCAGTGGAAATGATGA
CCGGTGCAACATGAAGAACAAATTCATTTGCAAATATTCTGATGAGAAACCAGCAGTTCCCT
CTAGAGAAGCTGAAGGTGAGGAAACAGAGCTGACAACACCTGTACTTCCAGAAGAAACACAG
GAAGAAGATGCCAAAAAAACATTTAAAGAAAGTAGAGAAGCTGCCTTGAATCTGGCCTACAT
CCTAATCCCCAGCATTCCCCTTCTCCTCCTCCTTGTGGTCACCACAGTTGTATGTTGGGTTT
GGATCTGTAGAAAAAGAAAACGGGAGCAGCCAGACCCTAGCACAAAGAAGCAACACACCATC
TGGCCCTCTCCTCACCAGGGAAAACAGCCCGGACCTAGAGGTCTACAATGTCATAAGAAAACA
AAGCGAAGCTGACTTAGCTGAGACCCGGCCAGACCTGAAGAATATTTCAATCCGAGTGTGTT
CGGGAGAAGCCACTCCCGATGACATGCTTGTGACTATGACAACATGGCTGTGAACCCATCA
GAAAGTGGGTTTGTGACTCTGGTGAGCGTGGAGAGTGGATTTGTGACCAATGACATTTATGA
GTTCTCCCCAGACCAATGGGGAGGAGTAAGGAGTCTGGATGGGTGGAAAATGAAATATATG
GTTATTAGGACATATAAAAACTGAAACTGACAACATGGAAAAGAAATGATAAGCAAAATC
CTCTTATTTTCTATAAGGAAAATACACAGAAGGTCTATGAACAAGCTTAGATCAGGTCCTGT
GGATGAGCATGTGGTCCCACGACCTCCTGTTGGACCCCCACGTTTTGGCTGTATCCTTTAT
CCCAGCCAGTCATCCAGCTCGACCTTATGAGAAGGTACCTTGCCAGGCTGGCACATAGTA
GAGTCTCAATAAATGTCACTTGGTTGGTTGTATCTAACTTTTAAGGACAGAGCTTTACCTG
GCAGTGATAAAGATGGGCTGTGGAGCTTGGAAAACCACTCTGTTTTCTTTCCTCTATACAG
CAGCACATATTATCATACAGACAGAAAATCCAGAACTCTTTCAAAGCCACATATGGTAGCACAG
GTTGCGCTGTGCATCGGCAATTCTCATATCTGTTTTTTTCAAAGAATAAAATCAAATAAAGA
GCAGGAAAAA

FIGURE 50

MRPGTALQAVLLAVLLVGLRAATGRLLSASDLDLRGGQPVCRRGGTQRPCYKVIYFHDTSRRL
NFEEAKEACRRDGGQLVSI ESEDEQKLEKFIENLLPSDGDWIGLRREEKQSNSTACQDL
YAWTDGSISQFRNWYVDEPSCGSEVCVVMYHQPSAPAGIGGPFYMQWNDDRCNMKNNFICKY
SDEKPAVPSREAEGEETELTTPVLPEETQEEDAKKTFKESREAAALNLAYILIPSIPLLLLLLV
VTTVVCVWWICRKRKREQDPSTKKQHTIWPSPHQGNSPDLEVYNVIRKQSEADLAETRPDL
KNISFRVCSGEATPDDMSCDYDNMAVNPSESGFVTLVSVESGFVTNDIYEFSPDQMGRSKES
GWVENEIYGY

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 117-121, 312-316

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 296-300

Casein kinase II phosphorylation site.

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,
299-303, 306-310, 323-327

N-myristoylation site.

amino acids 18-24, 37-43, 76-82, 146-152

FIGURE 51

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGGTCCCTGCTTGCTGAAGGGCTGGATGTACGC
ATCCGCAGGTTCCCGCGGACTTGGGGGCGCCCGCTGAGGCCCGCGCCGCGAGAAGACTTGT
GTTTGCTCTCTGCAGCCTCAACCCGAGGGGAGCGAGGGCCTACCACCATGATCACTGTTGT
GTTCAGCATGCGCTTGTGGACCCAGTGGGCGTCTGACCTCGCTGGCGTACTGCTTGCACC
AGCGGGCGGGTGGCCCTGGCCGAGCTGCAGGAGGCCGATGGCCAGTGTCCGGTCGACCGCAGC
CTGCTGAAGTTGAAAAATGTGTCAGGTCGTGTTTCGACACGGGGCTCGGAGTCCTCTCAAGCC
GCTCCCGCTGGAGGAGCAGGTAGAGTGAACCCCCAGCTATTAGAGGTCCCACCCCAAACCTC
AGTTTGATTACACAGTCAACCACTAGCTGGTGGTCCGAAACCATATTTCTCCTTACGACTCT
CAATACCATGAGACCACCTGAAGGGGGGCATGTTTGTCTGGGCAGCTGACCAAGGTGGGCAT
GCAGCAAATGTTTGCTTGGGAGAGAGACTGAGGAAGAACTATGTGGAAGACATTCCCTTTC
TTTCACCAACCTTCAACCCACAGGAGGTCTTTATTCGTTCCACTAACATTTTTCGGAATCTG
GAGTCCACCCGTTGTTTGTCTGGCTGGGCTTTTCCAGTGTGAGAAAGAAAGGACCATCATCAT
CCACACTGATGAAGCAGATTTCAGAAGTCTTGTATCCCACTACCAAAGCTGCTGGAGCCTGA
GGCAGAGAACCAGAGGCCGAGGCAGACTGCCTCTTTACAGCCAGGAATCTCAGAGGATTTG
AAAAAGGTGAAGGACAGGATGGGCATTGACAGTAGTGATAAAGTGGACTTCTTCATCCTCCT
GGACAACGTGGCTGCCGAGCAGGCACACAACCTCCCAAGCTGCCCCATGCTGAAGAGATTTG
CACGGATGATCGAACAGAGAGCTGTGGACACATCCTTGTACATACTGCCCAAGGAAGACAGG
GAAAGTCTTCAGATGGCAGTAGGCCCATTCCTCCACATCCTAGAGAGCAACCTGCTGAAAGC
CATGGACTCTGCCACTGCCCCGACAAGATCAGAAAGCTGTATCTCTATGCGGCTCATGATG
TGACCTTCATACCGCTCTTAATGACCTGGGGATTTTTGACCACAAATGGCCACCGTTTGCT
GTTGACCTGACCATGGAACCTTACCAGCACCTGGAATCTAAGGAGTGGTTTGTGCAGCTCTA
TTACCACGGGAAGGAGCAGGTGCCGAGAGGTTGCCTGATGGGCTCTGCCCGCTGGACATGT
TCTTGAATGCCATGTCACTTTATACCTTAAGCCAGAAAAATACCATGCACTCTGCTCTCAA
ACTCAGGTGATGGAAGTTGGAATGAAGAGTAACTGATTTATAAAGCAGGATGTGTTGATT
TTAAATAAAGTGCCCTTTATACAATG

FIGURE 52

MITGVFSMRLWTPVGVLTSLAYCLHQRRVALAELQEADGQCPVDRSLLKLKMVQVFRHGAR
SPLKPLPLEEQVEWNPQLLEVPPQTQFDYTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQL
TKVGMQQMFALGERLRKNYVEDIPFLSPTFNPQEVFIRSTNIFRNLESTRCLLAGLFQCQKE
GPIIIHTDEADSEVLYPNYQSCWSLRQRTGRRTASLQPGISEDLLKKVKDRMGIDSSDKVD
FFIILLDNVAAEQAHNLPSCPMLKR FARMIEQRAVDTSLYILPKEDRESLQMAVGPFHILES
NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLMTLGIFDHKWPPFAVDLTMELYQHLESKEW
FVQLYYHGKEQVPRGCPDGLCPLDMFLNAMS VYTLSPEKYHALCSQTQVMEVGNEE

Signal sequence:

amino acids 1-23

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 218-222

Casein kinase II phosphorylation site.

amino acids 87-91, 104-108, 320-324

Tyrosine kinase phosphorylation site.

amino acids 280-288

N-myristoylation site.

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

Amidation site.

amino acids 216-220

Leucine zipper pattern.

amino acids 10-32

Histidine acid phosphatases phosphohistidine signature.

amino acids 50-65

Abstract

TCCTCTTAAACATACATTGCAGCTAAAACATAAATTATGCTGCTTGGGGACCTCCTTCTAGCCT
TAAATTTTCAGCTCATCACCTTCACCTGCCTTGGTCAATGGCTCTGCTATTCTCCTTGATCCTT
GCCATTTGCACCAGACCTGGATTCTTAGCGTCTCCATCTGGAGTGCGGCTGGTGGGGGGCCT
CCACCGCTGTGAAGGGCGGGTGGAGGTGGAACAGAAAGGCCAGTGGGGCACCGTGTGTGATG
ACGGCTGGGACATTAAAGGACGTGGCTGTGTTGTGCGCGGAGCTGGGCTGTGGAGCTGCCAGC
GGAACCCCTAGTGGTATTTTGTATGAGCCACCAGCAGAAAAAGAGCAAAAGTCTCATCCA
ATCAGTCAGTTGCACAGGAACAGAAGATACATTGGCTCAGTGTGAGCAAGAAGAAGTTTATG
ATTGTTCAATGATGAAGATGCTGGGGCATCGTGTGAGAACCCAGAGAGCTCTTTCTCCCCA
GTCCAGAGGGTGTCAAGGCTGGCTGACGGCCCTGGGCATTGCAAGGGACGCGTGGAAAGTGAA
GCACCAGAACCAGTGGTATACCGTGTGCCAGACAGGCTGGAGCCTCCGGGCCGCAAAAGTGG
TGTGCCGGCAGCTGGGATGTGGGAGGGCTGTACTGACTCAAAAAACGTGCAACAAGCATGCC
TATGGCCGAGAAACCCATCTGGCTGAGCCAGATGTCTGCTCAGGACGAGAAGCAACCTTTCA
GGATTGCCCTTCTGGGCTTGGGGCGAAGAACACCTGCAACCATGATGAAGACAGTGGGTCTG
AATGTGAAGATCCCTTTGACTTGAAGCTAGTAGGAGGAGACAACCTCTGCTCTGGGCGACTG
GAGGTGCTGCACAAGGGCGTATGGGGCTCTGTCTGTGATGACAACTGGGCGAGAAAAGGAGGA
CCAGGTGGTATGCAAGCAACTGGGCTGTGGGAAGTCCCTCTCTCCCTCCTTCAGAGACCGGA
AATGCTATGCGCTGGGGTTGGCGCATCTGGCTGGATAATGTTGTTGTTGCTCAGGGGAGGAG
CAGTCCCTGGAGCAGTGCCAGCACAGATTTTGGGGGTTTACGACTGCACCCACCAGGAAGA
TGTGGCTGTCTCTGCTCAGTGTAGGTGGGCATCATCTAATCTGTTGAGTGCCTGAATAGAA
GAAAAACACAGAAGAAGGGAGCATTTACTGTCTACATGACTGCATGGGATGAACACTGATCT
TCTTCTGCCCTTGGACTGGGACTTATACTTGGTGCCCTGATTCTCAGGCCTTCAGAGTTGG
ATCAGAACTTACAACATCAGGTCTAGTTCTCAGGCCATCAGACATAGTTTGGAACTACATCA
CCACCTTTCTATGTCTCCACATTGCACACAGCAGATTCCCAGCCTCCATAATTGTGTGTAT
CAACTACTTAAATACATTCTCACACACACACACACACACACACACACACACACACATA
CACCATTGTCTGTTTCTCTGAAGAACTCTGACAAAATACAGATTTTGGTACTGAAAGAGA
TCTTAGAAGACCGAAATTTTAAAGGATAAATTTCTGAATTGGTTATGGGGTTTCTGAAATTG
GCTCTATAATCTAATTAGATATAAAATTTCTGGTAACTTTATTTACAATAATAAGATAGCAC
TATGTGTTCAA

FIGURE 54

MALLFSLILAICTRPGFLASPSGVRLVGGHLRCEGRVEVEQKGQWGTVCDDGWDIKDVAVLC
RELGCGAASGTPSGILYEPPAEKEQKVLIQSVSCTGTEDTLAQCEQEVEYDCSHDEDAGASC
ENPESSFSFVPEGVRLADGPGHCKGRVEVKHQNWYTVCTGWSLRAAKVVCRLGCGRAVL
TQKRCNKHAYGRKPIWLSQMSCSGREATLQDCPSGPGWKNTCNHDEDTWVECEDPFDLRLVG
GDNLCSGRLEVLHKGVWGSVCCDNWGEKEDQVCKQLGCGKSLSPSFRDRKCYGPGVGRIWL
DNVRCSGEEQSLEQCQHRFWGFDCTHQEDVAVICSV

Signal sequence:

amino acids 1-15

Casein kinase II phosphorylation site.

amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,
267-271, 294-298, 316-320, 336-340

N-myristoylation site.

amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,
180-186, 263-269, 286-292

Amidation site.

amino acids 196-200

Speract receptor repeated domain signature.

amino acids 29-67, 249-287

FIGURE 55

ACTGCACTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGAC
CCACGCGTCCGCGGACGCGTGGGCGGACGCGTGGGCCGGCTACCAGGAAGAGTCTGCCGAAG
GTGAAGGCCATGGACTTCATCACCTCCACAGCCATCCTGCCCCTGCTGTTGCGCTCCCTGGG
CGTCTTCGGCTCTTCCGGCTGCTGCAGTGGGTGCGCGGGAAGGCCTACCTGCGGAATGCTG
TGTTGGTGATCACAGGCGCCACCTCAGGGCTGGGCAAAGAATGTGCAAAAGTCTTCTATGCT
GCGGGTGCTAAACTGGTGCTCTGTGGCCGGAATGGTGGGGCCCTAGAAGAGCTCATCAGAGA
ACTTACCGCTTCTCATGCCACCAAGGTGCAGACACACAAGCCTTACTTGGTGACCTTCGACC
TCACAGACTCTGGGGCCATAGTTGCAGCAGCAGCTGAGATCCTGCAGTGCTTTGGCTATGTC
GACATACTTGTCAACAATGCTGGGATCAGCTACCGTGGTACCATCATGGACACCACAGTGGA
TGTGGACAAGAGGGTCATGGAGACAACTACTTTGGCCAGTTGCTCTAACGAAAGCACTCC
TGCCCTCCATGATCAAGAGGAGGCAAGGCCACATTGTGCGCCATCAGCAGCATCCAGGGCAAG
ATGAGCATTCCTTTTCGATCAGCATATGCAGCCTCCAAGCACGCAACCCAGGCTTTCTTTGA
CTGTCTGCGTGCCGAGATGGAACAGTATGAAATTGAGGTGACCGTCATCAGCCCCGGCTACA
TCCACACCAACCTCTCTGTAAATGCCATCACCGCGGATGGATCTAGGTATGGAGTTATGGAC
ACCACCACAGCCCAGGGCCGAAGCCCTGTGGAGGTGGCCAGGATGTTCTTGTCTGCTGTGGG
GAAGAAGAAGAAAGATGTGATCCTGGCTGACTTACTGCCTTCCTTGGCTGTTTATCTTCGAA
CTCTGGCTCCTGGGCTCTTCTTCAGCCTCATGGCCTCCAGGGCCAGAAAAGAGCGGAAATCC
AAGAACTCCTAGTACTCTGACCAGCCAGGGCCAGGGCAGAGAAGCAGCACTCTTAGGCTTGC
TTACTCTACAAGGGACAGTTGCATTTGTTGAGACTTTAATGGAGATTGTCTCACAAAGTGGG
AAAGACTGAAGAAACACATCTCGTGCAGATCTGCTGGCAGAGGACAATCAAAAACGACAACA
AGCTTCTTCCAGGGTGAGGGGAAACCTTAAGGAATAAATATGGAGCTGGGGTTAACT
AAAACTAGAAATAAACATCTCAACAGTAAAAAAAAAAAAAAAAAGGGCGGCCGCACTTAG
AGTCGACCTGCAGAAGCTTGGCCGCATGGCCCAACTTGTATTATGCAGCTTATAATGGTTAC

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FIGURE 56

MDFITSTAILPLLFGCLGVFGLFRLLQWVRGKAYLRNAVVTGATSGLGKECAKVFYAAGA
KLVLGCRNGGALBELIRELTASHATKVQTHKPYLVTFDLTDSGAIVAAAAEILQCFGYVDIL
VNNAGISYRGTIMDITVDVDKRVMETNYFGPVALTKALLPSMIKRRQGHIVAISISIQKMSI
PFRSAYAASKHATQAFFDCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDTTT
AQGRSPVEVAQDVLAAVGKKKKDVLADLLPSLAVYLRTLAPGLFFSLMASRARKERKSKNS

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 104-120, 278-292

N-glycosylation site.

amino acids 228-232

Glycosaminoglycan attachment site.

amino acids 47-51

Casein kinase II phosphorylation site.

amino acids 135-139, 139-143, 253-257

Tyrosine kinase phosphorylation site.

amino acids 145-153, 146-153

N-myristoylation site.

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

Amidation site.

amino acids 265-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 6-17

FIGURE 58

MKFLLDILLLLPLLVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK
LVLWDINKHGLEETAACKCKGLGAKVHTFVVDCSNREDIYSSAKVKAEIGDVSILVNNAGVV
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHI VTVASAAGHVSVPFLLAYC
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVVNRLMH
GILTEQKMFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMQ

Signal sequence:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-34, 283-287

Casein kinase II phosphorylation site.

amino acids 52-56, 95-99, 198-202, 267-271

N-myristoylation site.

amino acids 43-49, 72-78, 122-128, 210-216

FIGURE 60

MVGAMWKVIVSLVLLMPGPCDGLFRSLYRSVSMPPKGDGQPLFLTPYIEAGKIQKGRELSL
VGPFPGNLNMSYAGFLT VNKTYNSNLF FWF FPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEH
GPYVVT SNMTRLRDRFPWTTTLSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLYSALIQT
FQIFPEYKNNDFYVTGESYAGKYVPAIAHLIHSNLPVREVKINLNGIAIGDGYSDPESIIG
YAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEAFEILDKLLDGLTSDPSYFQNVGT
CSNYYNFLRCTEPEDQLYYVKFLSLPEVRQAIHVGNQTFNDGTIVEKYLREDTVQSVKPWLT
EIMNNYKVLINQQLDII VAAALTE RSLMGMDWKGSGQEYKKAEEKVWKIFKSDSEVAGYIRO
AGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYKGWDPPYVG

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 81-85, 132-136, 307-311, 346-350

Casein kinase II phosphorylation site.

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,
353-357, 424-428

Tyrosine kinase phosphorylation site.

amino acids 423-432

N-myristoylation site.

amino acids 22-28, 110-116, 156-162, 232-238

Serine carboxypeptidases, serine active site.

amino acids 200-208

Crystallins beta and gamma 'Greek key' motif signature.

amino acids 375-391

FIGURE 61

CGAGGGCTTTTCCGGCTCCGGAATGGCACATGTGGGAATCCCAGTCTTGTGTGGCTACAACAT
 TTTTCCCTTTCCCTAACAGTTCTAACAGCTGTCTAACAGCTAGTGATCAGGGGTTCTTCTT
 GCTGGAGAGAAAGGGCTGAGGGCAGAGCAGGGCACTCTCACTCAGGGTGACCAGCTCCCTTG
 CCTCTCTGTGGATAACAGAGCATGAGAAAGTGAAGAGATGCAGCGGAGTGAGGTGATGGAAG
 TCTAAAATAGGAAGGAATTTTGTGTGCAATATCAGACTCTGGGAGCAGTTGACCTGGAGAGC
 CTGGGGGAGGGCTGCCTAACAGCTTCAAAAAACAGGAGCGACTTCCACTGGGCTGGGAT
 AAGACGTGCGGTAGGATAGGGAAGACTGGGTTTAGTCTCTAATATCAAATTGACTGGCTGGG
 TGAACCTCAACAGCCTTTTAACTCTCTGGGAGATGAAAAACGATGGCTTAAGGGGCCAGAAA
 TAGAGATGCTTTGTAAAAATAAAATTTTAAAAAAAGCAAGTATTTTATAGCATAAAGGCTAGA
 GACCAAAATAGATAACAGGATTCCCTGAACATTCCTAAGAGGGAGAAAGTATGTTAAAAATA
 GAAAAACCAAAATGCAGAAGGAGGAGACTCACAGAGCTAAACAGGATGGGGGACCTTGGGTC
 AGGCCAGCCTCTTTGCTCCTCCCGAAATTATTTTGGTCTGACCACTCTGCCTTGTGTTTT
 GCAGAATCATGTGAGGGCCAAACGGGGAGGTTGGAGCAGATGAGCACACAGGAGCCGCTCT
 CCTCACCGCCGCCCTCTCAGCATGGAAACAGGGCAGCCCTGGCCCGGGCCCTGGAGGTGG
 ACAGCCGCTCTGTGTCCTGCTCTCAGTGGTCTGGGTGCTGCTGGCCCCCAGCAGCCGGC
 ATGCTCAGTTTCAGCACCTTCCACTCTGAGAATCGTGAAGTGGACCTTCAACCACCTTGACCGT
 CCACCAAGGGCAGGGGGCGCTCTATGTGGGGCCATCAACCGGCTCTATAAGCTGACAGGCA
 ACCTGACCATCCAGTGGCTCATAGAAGCAGGGCCAGAAGGAGCAACAAGTCTCGTTACCCG
 CCCCTCATCGTGAGCCCTGACGCAAGTGCTCACCTCACCAACATGTCAACAGCTGCT
 CATCATGACTACTCTGAGAACCGCTGCTGGCCTGTGGGAGCCTCTACCAGGGGGTCTGCA
 AGCTGCTGCGGCTGGATGACCTCTTCTCTGCTGGTGGAGCCATCCCACAAGAGGAGCACTAC
 CTGTCCAGTGTCAACAAGACGGGCACCATGTACGGGGTATTGTGCGCTCTGAGGGTGAGGA
 TGGCAAGCTCTTATCGGCACGGCTGTGGATGGGAAGCAGGATTACTTCCCGACCTGTCCA
 GCCGGAAGCTGCCCGAGACCTGAGTCTCAGCCATGCTCGACTATGAGCTACACAGCGAT
 TTTGCTCCTCTCTCATCAAGATCCCTTCAGACACCCCTGGCCCTGGTCTCCCACCTTGACAT
 CTTCTACATCTACGGCTTTGCTAGTGGGGCTTTGTCTACTTTCTCACTGTCCAGCCCGAGA
 CCCCTGAGGGTGTGGCCATCAACTCCGCTGGAGACCTTCTTACACCTCAGCATCGTGGCG
 CTTCTGAAGGATGACCCCAAGTTCCACTCATACGTGTCCTGCGCTTGGCTGCACCCGGGC
 CGGGGTGGAATACCGCCTCCTGCAGGCTGCTTACCTGGCCAAGCCTGGGGACTCACTGGCCC
 AGGCCTTCAATATCACAGCCAGGACGATGTACTCTTTGCCATCTTCTCAAAAGGCGAGAAG
 CAGTATCACCAACCCGCGGATGACTCTGCCCTGTGTGCTTCCCTATCCGGGCCATCAACT
 GCAGATCAAGGAGCGCTGAGTCTCTGCTACCAGGCGAGGCAACCTGAGACTCAACTGGC
 TGTGGGGAAGGACGTCCAGTGACAGAAAGGCGCTGTCCCCATCGATGATAACTCTGTGGA
 CTGGACATCAACAGCCCTCGGGAGGCTCAACTCCAGTGGAGGGCCTGACCTGTACACCA
 CAGCAGGACCGCATGACCTCTGTGGCCTCTACGTTTACAACGGCTACAGCGTGGTTTTG
 TGGGACATAAGAGTGGCAAGCTGAAAAAGGTAAAGAGTCTATGAGTTCAGATGCTCCAATGCC
 ATTCACTCTCAGCAACAGAGTCCCTCTTGGAAAGGTAGCTATTGGTGGAGATTTAACTATAG
 GCAACTTTATTTCTTGGGGAACAAGGTGAATGGGGAGGTAAGAAGGGGTAAATTTTGTG
 ACTTAGCTCTAGCTACTCTCTCCAGCCATCAGTCATTGGGTATGTAAGGAATGCAAGCGTA
 TTTCAATATTTCCAACTTTAAGAAAAACTTTAAGAAGGTACATCTGCAAAAGCAA

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FIGURE 62

MGTILGQASLFAPPNGYFWS DH S A L C F A E S C E G Q P G K V E Q M S T H R S R L L T A A P L S M E Q R Q P W P
R A L E V D S R S V V L L S V V W V L L A P P A A G M P Q F S T F H S E N R D W T F N H L T V H Q G T G A V Y V G A I N R V
Y K L T G N L T I Q V A H K T G P E E D N K S R Y P P L I V Q P C S E V L T L T N N V N K L L I I D Y S E N R L L A C G S L
Y Q G V C K L L R L D D L F I L V E P S H K K E H Y L S S V N K T G T M Y G V I V R S E G E D G K L F I G T A V D G K Q D Y
F P T L S S R K L P R D P E S S A M L D Y E L H S D F V S S L I K I P S D T L A L V S H F D I F Y I Y G F A S G G F V Y F L
T V Q P E T P E G V A I N S A G D L F Y T S R I V R L C K D D P K F H S Y V S L P F G C T R A G V E Y R L L Q A A Y L A K P
G D S L A Q A F N I T S Q D D V L F A I F S G Q K Q Y H H P P D D S A L C A F P I R A I N L Q I K E R L Q S C Y Q G E G N
L E L N W L L G K D V Q C T K A P V P I D D N F C G L D I N Q P L G G S T P V E G L T L Y T T S R D R M T S V A S Y V Y N G
Y S V V F V G T K S G K L K K V R V Y E F R C S N A I H L L S K E S L L E G S Y W W R F N Y R Q L Y F L G E Q R

Signal sequence:

amino acids 1-32

Transmembrane domain:

amino acids 71-87

N-glycosylation site.

amino acids 130-134, 145-149, 217-221, 381-385

Casein kinase II phosphorylation site.

amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,
384-388, 471-475, 481-485, 530-534

N-myristoylation site.

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

FIGURE 63

AGGCTCCCGCGCGGGCTGAGTGCAGGACTGGAGTGGGAACCCGGGTCCCCGCGCTTAGAGAACACCGGATGA
 CGTGGAGCCTCCGGCGAGGCCGGCCCGCAGCTGGAGACTCTGCTGCTGGTGTCTTTGGGCTTCTTGGTCTCC
 GCAGGCTGGACTGGAGCACCTGGTCCCTCTGCGGCTCCGCCATCGACAGCTGAGGGCTGAGGCCAAGGGCTGGA
 ACTTCTATGCTGGAGGATTCACCTTCTGGATCTTCGGGGGCTCCATCTACCTATTTCCGTGTGCCAGGGAGTCT
 GAGGGACCGGCTGTGAAGATGAAGGCCCTGGGCTTGAACACCTTACCACCTATGTTCCTGGGAACCTGCATG
 AGCCAGAAAGAGGCAAAATTTGACTTCTCTGGGAACCTGGACCTGGAGGCTTCGTCCTGATGGCCGACAGATCG
 GGCTGTGGGTGATTCTGGCTCCAGGCCCTACATCTGCAGTGAATGGACCTTCGGGGCTTGCCCAAGCTGCTAC
 TCCAGAGCTCTGGCATGAGGCTGAGGACAACTTACAAGGGCTTACCAGAGCAGTGGACCTTTATTTTGGACACC
 TGATGTCCAGGGTGGTGCCACTCCAGTACAAGCGTGGGGGACCTTATCTGGCTGAGGTGAGAGATGAATATG
 GTTCTATAAAGACCCGCATACATGCCCTACGTCAGGAAGGCACTGGAGGACCTGGGCATTGTGGAACCTGC
 TCTGACTTCAGACAAAGGATGGGCTGAGCAAGGGGATGTCCAGGGAGCTTGGCCACCATCAACTTGCATG
 CAACACACAGGCTGCAGCTACTGACCACTTCTCTTCAAGCTCCAGGGGACTCAGCCCAAGATGGTGATGGAGT
 ACTGGACGGGGTGGTTGACTCGTGGGGAGGCCCTCAATATCTTGGATTCTCTGAGGTTTTGAAAACCGTGT
 CTGCCATGTGGACCGCGGCTCTCCATCAACCTCTACATGTTCCAGGAGGCCAACACTTTGGCTTCATGAATG
 GAGCCATGCACCTCCATGACTACAAGTCAGATGTACAGCTATGACTATGATGCTGTGCTGACAGAAGCCGGCG
 ATTAACAGGCCAAGTACATGAAGCTTCGAGACTTCTTCGGCTCCATCTCAGGCACTCCCTCTCCCTCCCCACCTG
 ACCCTCTTCCCAAGATGCCGTATGAGCCCTTAACGCCAGTCTTGTACCTGTCTCTGTGGGACGCCCTCAAGTACC
 TGGGGGAGCCAATCAAGCTGAAAAGCCCATCAACATGGAGAACCTGCCAGTCAATGGGGGAATGGCAGACTCCT
 TCGGGTACATTTCTATGAGACAGCATCACTCGTCTGGCATCCTCAGTGGCCACGCTGCATGATCGGGGCGAGG
 TGTTTGTGAACACAGTATCCATAGGATTCTTGGACTACAAGACAAACGAAGATTGCTTCCCTGATCCAGGGTT
 ACACCGTGCTGAGGATCTTGGTGGAATCGTGGCGAGTCAACTATGGGAGAAATATTGATGACAGCGCAAAG
 GCTTAATTTGAAATCTCTATCTGAATGATTACCCCTGAAAACCTTCAAGATCTATAGCTCGGATATGAAGAAGA
 GCTTCTTTAGAGGTTGGGCTGGACAAATGNGNTTCCCTCCAGAAACACCCACATTAAGCTGCTTTCTTTGG
 GTAGCTTGTCCATCAGCTCCAGCGCTTGTGACACCTTTCTGAAGCTGGAGGCTGGGAGAGGGGGTGTATTA
 TCAATGGCCAGAACCTTGGAGCTTACTGGAACATTGGAACCCAGAAAGCGCTTTACCTCCAGGTCCTGGTTGA
 GCAGCGGAATCAACAGGTCTATCGTTTGAAGAGACGATGGCGGCTGGCACCCCTCTGCTGGTGCCAGTGGGAGATGCGCGCTC
 ACTTGGGCGAGAACCAAGTACATTAAGTGAAGCGTGGCAGCCCTCTGCTGGTGCCAGTGGGAGATGCGCGCTC
 CTCCTTGAACCTGAAGCTGGTGGCTGCTGCCCCACCCCTCACTGCAAAAGCATCTCTTAAGTAGCAACCTCAGG
 AGCTAATCAGATCGCCAGCCTTTGGCCCTCAGAAAAAGTGTGAAACGTGCCCTTGACCGGAGCGTCACAGCCC
 TGGCTTTGTGATGATGGCTTCTTACAGCCCTGCTTGTGCGGAGGCTGCTGGGCTGTCTTATAGGAGTGGGAGC
 TTTATCCCGAAATCTGGGTGTGTCACAGTGTAGAGGCTGGGGAAGGGGTGTCTCACTGAGCTGACTTTGTT
 CTTCCTTCAACACTTCTGAGCCTTCTTGGGATTCTGGAAGGAATCTCGGCTGAGAAACATGTGACTTCCCTT
 TCCCTTCCACTCGCTGCTTCCACAGGGTGACAGGCTGGGCTGGAGAAACAGAAATCTTCAACCTCGCTTCC
 CAACTTAGCAGTGTCTCTGGTGTGAGTGAGGAGGACATGTGAGTCTTGGCAGAAGCCATGGCCCATGTCTGCATCC
 CATCCAGGAGGAGGAGCAGAAGGCCAGCTCACATGTGAGTCTTGGCAGAAGCCATGGCCCATGTCTGCATCC
 AGGAGGAGGAGCAGAAGGCCAGCTCACATGTGAGTCTTGGCAGAAGCCATGGCCCATGTCTGCATCCAGGAGG
 ACAGAAGGCCAGCTCAGTGGGCCCTTCCACCCCAAGCCGGAACAGCAGGAGGAGGAGGAGGAGGAGGAGG
 GAAGTGTGTCAGGTCGAGCTTGTAGCTTGTCTGGGGCCAGGCCAACCTTGGCTTGGGCTCAGTGTCTGTA
 GTTGCAGTAAAGCTATAACCTGAATCACAA

00004333.071201

FIGURE 64

MTTWSLRRRPARTLGLLLLVVLGFLVLRRLDWS TLVPLRLRHRQLGLQAKGWNFMLEDSTFW
IFGGSIH YFRVPREYWRDRLLKMKACGLNTLT TYVPWNLHEPERGKFD FSGNLDLEAFV LMA
AEIGLWVILRPGPYICSEMDLGG LPSWLLQDPGMR LRTTYKGFT EAVDLYFDH LMSRVVPLQ
YKRGGPIIAVQVENEYGSYNKDPAYMPYVKKALEDRGIVE LLLTSDNKG LSKGIVQGV L AT
INLQSTHELQ LLLTTF LFNVQGTQPKMVMEYWTGW FDSWGGPHN ILDSSEVLKTVSAI VDAGS
SINLYMFHGGTNFGFMNGAMHFDYKSDVTSYDYDAVLTEAGDYTA KYMKLRDFFGSISGIP
LPPPPDLLPKMPYEPLTPVLYLSLWDALKYLGEPIKSEKPINMENLPVNGNGQSF GYI IYE
TSITSSGILSGHVHDRGQVFVNTV SIGFLDYKTTKIAVPLIQGYTVLRILVENRGRVNYGEN
IDDQRKGLIGNLYLNDSP LKNFRIYS LDMKKSFFQRFG LDKWXS L PETPTLP AFFLGSLSIS
STPCDTFLKLEGWEKG VVFINGQNLGRYWNIGPQKTLYLPGPW LSSGINQVIVFEETMAGPA
LQFTETPHLGRNQYIK

Signal sequence:

amino acids 1-27

Casein kinase II phosphorylation site.

amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

N-myristoylation site.

amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586

FIGURE 66

MAPKKLSCLRSLLLPLSLTLLLPQADTRS FVVD RGHDRFLLDGAPFRYVSGSLHYFRVPRVL
WADRLLKMRWSGLNAIQFYVPWNYHEPQPGVYNFNGSRDLIAFLNEAALANLLVILRPGPYI
CAEWEMGGLPSWLLLRKPEIHLRTSDPDFLAAVDSWFKVLLPKIYPWLYHNGGNIISIQVENE
YGSYRACDFSYMRLAGLFRALLGEKILLFTTDDGPEGLKCGSLRGLYTTVD FGPADNMTKIF
TL LRKYE PHGPLVNSEYYTGWLDYWGQNHSTRSVSAVTKGLENMLKLGASVNMYMFHGGTNF
GYWNGADKKGRFLPITTSYDYDAPISEAGDPTPKLFALRDVISKFQEVPLGPLPPSPKMML
GPVTLHLVGHLLAFLDLLCPRGPIHSILPMTFEAVKQDHGFMLYRTYMTHTIFEPTPFWVPN
NGVHDRAYVMVDGVFQGVVERNMRDKLFLTGKLGSKLDILVENMGRLSFGSNS SDFKGLLKP
PILGQTILTQWMMFPLKIDNLVKWWFPLQLPKWPYPQAPSGPTFYSKTFPILGSVGDTFLYL
PGWTKGQVWINGFNLGRYWTKGFPQQTLYVPRFLLFPRGALNKITLLELEDVPLQPQVQFLD
KPILNSTSTLHRTHINSLSADTLSASEPMELSGH

Signal sequence:

amino acids 1-27

N-glycosylation site.

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 4-8

Casein kinase II phosphorylation site.

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,
603-607, 644-648

Tyrosine kinase phosphorylation site.

amino acids 191-198

N-myristoylation site.

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

FIGURE 67

GCTTTGAACACGTCTGCAAGCCCAAAGTTGAGCATCTGATTGGTTATGAGGTATTTGAGTGC
ACCCACAATATGGCTTACATGTTGAAAAAGCTTCTCATCAGTTACATATCCATTATTTGTGT
TTATGGCTTTTATCTGCCTCTACACTCTCTTCTGGTTATTTCAGGATACCTTTGAAGGAATATT
CTTTCGAAAAAGTCAGAGAAGAGAGCAGTTTTAGTGACATTCCAGATGTCAAAAACGATTTT
GCGTTCCTTCTTTCACATGGTAGACCAGTATGACCAGCTATATTCCAAGCGTTTTGGTGTGTT
CTTGTCAGAAGTTAGTGAAAAATAAACTTAGGGAATTAGTTTGAACCATGAGTGGACATTTG
AAAAACTCAGGCAGCACATTTACGCAACGCCAGGACAAGCAGGAGTTGCATCTGTTTCATG
CTGTCGGGGGTGCCCGATGCTGTCTTTGACCTCACAGACCTGGATGTGCTAAAGCTTGAAC
AATTCAGAAGCTAAAAATTCCTGCTAAGATTTCTCAAATGACTAACCTCCAAGAGCTCCACC
TCTGCCACTGCCCTGCAAAAGTTGAACAGACTGCTTTTAGCTTTCTTCGCGATCACTTGAGA
TGCCTTCACGTGAAGTTCACTGATGTGGCTGAAATTCCTGCCTGGGTGTATTTGCTCAAAAA
CCTTCGAGAGTTGTACTTAATAGGCAATTTGAACTCTGAAAACAATAAGATGATAGGACTTG
AATCTCTCCGAGAGTTGCGGCACCTTAAGATTCTCCACGTGAAGAGCAATTTGACCAAAGTT
CCCTCCAACATTACAGATGTGGCTCCACATCTTACAAAGTTAGTCATTATAATGACGGCAC
TAAACTCTTGGTACTGAACAGCCTTAAGAAAATGATGAATGTCGCTGAGCTGGAACCTCAGA
ACTGTGAGCTAGAGAGAATCCACATGCTATTTTCAGCCTCTCTAATTTACAGGAACCTGGAT
TTAAAGTCCAATAACATTGCGACAATTGAGGAAATCATCAGTTTCCAGCATTTAAACGACT
GACTTGTTTAAATATGGCATAACAAAATTGTTACTATTCTCTCTATTACCCATGTCA
AAAAGTTGGAGTCACTTTATTTCTTAACAACAAGCTCGAATCCTTACCAGTGGCAGTATTT
AGTTTACAGAACTCAGATGCTTAGATGTGAGCTACAACAACATTTCAATGATTCCAATAGA
AATAGGATTGCTTCAGAACCTGCAGCATTTCATATCACTGGGAACAAAGTGGACATTTCTGC
CAAAACAATTTGTTTAAATGCATAAAGTTGAGGACTTTGAATCTGGGACAGAAGTGCATCACC
TCACTCCCAGAGAAAGTTGGTCAGCTCTCCAGCTCACTCAGCTGGAGCTGAAGGGGAAGTGC
CTTGAGACCGCTGCCAGCCAGCTGGGCCAGTGTGGATGCTCAAGAAAAGCGGCTTGTG
TGGAAGATCACCTTTTGTATACCCTGCCACTCGAAGTCAAAGAGGCATTGAATCAAGACATA
AATATTCCCTTTGCAATGGGATTTAAACTAAGATAATATATGCACAGTGATGTGCAGGAAC
AAGTTCCTAGATTGCAAGTGCTCACGTACAAGTTATTACAAGATAATGCATTTTAGGAGTAG
ATACATCTTTTAAAAATAAAAAGAGAGGATGCATAGAAGGCTGATAGAAGACATAACTGAAT
GTTCAATGTTTGTAGGTTTTTAAGTCATTCAATTTCCAAATCATTTTTTTTCTTTTGGGG
AAAGGGAAGGAAAAATTATAATCACTAATCTTGGTCTTTTTTAAATGTTTGTAACTTGGAT
GCTGCCGCTACTGAATGTTTACAAATGCTTGCTGCTTAAAGTAAATGATTAAATTGACATT
TTCTTACTAAAAA

FIGURE 68

MAYMLKKLLISYISIIICVYGFCILYTLFWLFRIPRLKEYSFEKVBREESSFSDIPDVKNDF AFL
LHMVDQYDQLYSKRFGVFLSEVSENKLR EISLNHEWTFEKL RQHISRNAQDKQELHFLM LSG
VPDAVFDLTDLDVLKLEL IPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFLRDHLRCLH
VKFTDVAEIPAWVYLLKNLRELYLIGNLSEN NKMIGLESRLREL RHLKILHVKS NLT KVPSN
ITDVAPHLTKLVIHNDG TKLLVLNSLKKMMNVAE LELQNC ELERIPHAIFSLSNLQELDLKS
NNIRTIEBIIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLES LYFSNNKLES LPVAVFSLQ
KLRC LDVS YNNISM IPIEIGLLQNLQHLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLP
EKVGQLS QLTQLELKGNC LDR LPAQLGQC RMLKKSGLVVEDH LFD TLPLEVKEALNQDINIP
FANGI

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 241-245, 248-252, 383-387

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 326-330

Casein kinase II phosphorylation site.

amino acids 48-52, 133-137, 226-230, 315-319, 432-436, 444-448

Tyrosine kinase phosphorylation site.

amino acids 349-355, 375-381

N-myristoylation site.

amino acids 78-84, 124-130, 212-218, 392-398

FIGURE 69

CCCACGCGTCCGGCCTTCTCTCTGGACTTGCATTTCCATTCCCTTTTCATTGACAAACGTACTTTTTTATTTCT
 TTTTTTCCATCTCTGGCCAGCTTTGGGATCCTAGGCCGCCCTGGGAAGACATTTGTGTTTTACACACATAGGAT
 CTGTGTTTGGGGTTTCTTCTTCTCCCTGCATTTGGCATTTGCTTAGTGGTTGTGTGGGAGGGAGCCACCTGG
 GCTCAGTGGTCTGCTTGCATTTATCTGCTTAGGTACATCTGAAGTCTTTTGACCTCCATACAGTGATTTATGCCCTGTC
 ATCCCTGGTGGTATCCTGGCGGCTTGTCTCTGCTGATAGTTGTGCTGCTCTGTCTTTACTTCAAATAACACAAAC
 GCGCTAAAAGCTGCAAAAGGAACCTGAAGCTGTGGCTGTAAAAATCACACACCAGACAGAGGTGTGGTGGGCCAAG
 AACAGCCAGGCCAAAACCATTTGCCACGGAGTCTTTGCTCGCCTGCAAGTGTGTGAAGGATATAGAATGTGTGCC
 AGTTTTGATCTCCTGCCACTCTGCTGTGCGACATAAATGAGGGCTCTGTAGTTAGGAAAGGCTCCCTTCTCAA
 GCAGAGCCTTGAAGACTTCAATGATGTCAATGAGGCCACCTGTTTGTGATGTGCAGGACAGAAAGGACAG
 CTCCTCCATCAGTTTCATGGAATAAATCAGTGCCCTGTGGGAACAGCTGTGGAGATCCCTACAGAGAGCTTC
 CACTGGGGGCAACCTTCCAGGAAGGAGTTGGGGAGAGAGAACCTCACTGTGGGGAATGCTGATAAACCAAGTCA
 CACAGCTGTCTATTCTCACACAAATCTACCCCTTGCCTGTGCTGGAAGTCAAGTTCCTTGGAGGTGTCCAGAAA
 GCTGATGTAAACAGAGCCTATAAAAGCTGTGCTCTCTTAAGGCTGCCAGCGCTTGCCAAAATGGAGCTTGTA
 AGAAGGCTCATGCCATTGACCTCTTAAATCTCTCTGTTTGGCGGAGCTGACAAATGGCGGAGGCTGAAGGCAAT
 GCAAGCTGCACAGTCACTAGGGGGTGCCAAATATGGCAGAGACCCACAAAGCCATGATCTGCAACTCAATCCC
 AGTGAGAACTGCACCTGGACAAATAGAAAGACAGAAAAACAAAGCATCAGAATTATCTTTTCTATGTCCAGCTT
 GATCCAGATGGAAGCTGTGAAAGTGAAGACATTAAGTCTTTGACGGAACCTCCAGCAATGGGCCCTCTGCTAGGG
 CAAGTCTGCAGTAAAAACGACTATGTCTCTGATTTGAATCATCATCAGTACATTGACGTTTCAAAATAGTTACT
 GACTCAGCAAGAAATCAAAGAACTGTCTTTGTCTTCTACTACTTCTTCTCTCTTAACATCTCTATTCCAACTGT
 GGGCGTTTACCTGGATACCTTGGAAAGATCCTTACCAGGCCCAATTACCACAAAGCCGACTCTGAGCTGGCTTAT
 TGTGTGTGGCACATACAAGTGGAGAAAGATTACAAGATAAACTAAACTCAAAGAGATTTTCTAGAAATAGAC
 AAACAGTGCAAAATTTGATTTTCTGCCATCTATGATGGCCCTCCACCAACTCTGGGCTGATTGGACAAAGTCTGT
 GGCCGTGTGACTCCCACTTCAAGTCAATCGTCACTCAAACCTCTGACTGTGCTGTGTGCTACAGATTATGCCAATTCT
 TACCGGGATTTTCTGCTTCTCACTCACTCAATTTATGACAGAAACATCAACACTACATCTTTAACTTGCTCTTCT
 GACAGGATGAGAGTTATTATAAGCAAAATCTTACCTAGAGGCTTTTAACTCTAATGGGAATTAACCTGCAACTAAAA
 GACCAACTTGCAGACCAAAATTTATCAAATGTTGTGGAATTTCTGCTCCTCTTAATGGATGTGGTACAACTGAG
 AAGGTAGAAGATCAGTCAATTACTTACACCAATATAATCACTTTTCTGCACTTCACTCACTTGTGAAGTATCAAC
 CGTCAGAAACAACTCCAGATTATTGTGAAGTGTGAATGGGACATAATTTCTACAGTGGAGATTAATATACATAACA
 GAAGATGATGTAATCAAAGTCAAATGCACTGGGCAATATAACACCAAGTGGCTCTTTTGAATCCAAATTTCA
 TTTGAAAGAATATACTTGAATCACCATATTAATGTGGAATTTGAACCAAACTCTTTTGTGTAAGTTAGCTCTGCAC
 ACCTCAGATCCAAATTTGGTGGTGTCTTCTTGATACCTGTAGAGCCTCTCCACCTCTGACTTGTGATCTCCAAGT
 TACGACCTTAATCAGAGTGGAGTGTAGTGCAGATGAAACTTGAAGTGTATCCCTTATTTGGACATATAGGGAGA
 TTTCAAGTTAATGCTTTAAATTTCTTGAAGATGAGCTCTGCTGATCTGCAGTGATAAGTTTTGATATGTGAT
 AGCAGTGACCAACAGTCTCTGCTGCAATCAAGGTGTGCTCCAGAAGCAACAGAGATTTCTCATATAAATGG
 AAAACAGATTCCATCATAGAGCCCATTTGCTCTGAAAGGGATCGAAGTCAAGTGGCAATTCAGGATTTAGCAGAT
 GAAACACATGCGGAAGAAACTCCAAACAGCCTTTCAACAGTGTGATCTGTTTTTCTCTCATGTTCTAGCTCTG
 AATGTGTGACTGTAGCAGCAATCAAGTGAAGCAATTTTGAATCAACGGGCAGACTACAAATCAACAGAGCTG
 CAGAACTATTAACTAACAGTCCAACTTAAAGTGAAGCATGTTTCTCAGGATGCCAAAGGAATGCTACCTCTG
 GGCTACACATATTATGAATAAATGAGGAAGGGCTGAAAGTGACACAGGCCCTGCATGTAAAAAA

FIGURE 70

MELVRRRLMPLTLILLSLAELTMAEAEGNASCTVSLGGANMAETHKAMILQLNPSENCWTI
ERPENKSIRIIFSVYQLDPDGSCSEENIKVFDGTSSNGPILGQVCCKNDYVPVFESSSSTLT
FQIVTDSARIQRTVFVFFYFFSPNISIPNCGGYLDTLEGSFTSPNYPKPPELAYCVWHIQV
EKDYKIKLNFKEIFLEIDKQCKFDFLAIYDGPSTNSGLIGQVCGRVTPTFESSSNSLTVVLS
TDYANSYRGFSASYTSIYAENINTTSLTCSSDRMRVIIISKYLEAFNSNGNNLQLKDPTCRP
KLSNVVEFSVPLNGCGTIRKVEDQSITYTNIITFSASSTSEVITRQKQLQIIIVKCEMGNST
VEIIYITEDDVIQSQNALGKYNTSMALFESNSFEKTILESPPYYVDLNQTLFPVQVSLHTSDPN
LVVFLDTCRASPTSDFASPTYDLIKSGCSRDETCKVYPLFGHYGRFQFNAFKFLRSMSSVYL
QCKVLICDSDHQSRCNQGCVSRSKRDISSYKWKTDSSIIGPIRLKRDRSASGNSGFQHETHA
EETPNQPFNSVHLFSFMVLALNVVTATITVRHFVNQRADYKYQLQNY

Signal sequence:

amino acids 1-24

Transmembrane domain:

amino acids 571-586

N-glycosylation site.

amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,
394-398, 419-423

Casein kinase II phosphorylation site.

amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,
408-412, 463-467, 520-524, 556-560

Tyrosine kinase phosphorylation site.

amino acids 172-180, 407-415, 407-416, 519-528

N-myristoylation site.

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 71

GACGGAAGAACAGCGCTCCCGAGGCCGCGGGAGCCTGCAGAGAGGACAGCCGGCCTGCGCCG
 GGACATGCGGCCCCAGGAGCTCCCCAGGCTCGCGTTCCCGTTGCTGCTGTTGCTGTTGCTGTC
 TGCTGCCGCCGCCGCCGCTGCCCTGCCACAGCGCCACGCGCTTCGACCCCACTGGGAGTCC
 CTGGACGCCCCGCCAGCTGCCCGCGTGGTTTGACCAGGCCAAGTTCGGCATCTTCATCCACTG
 GGGAGTGTTCCTCGTGCCAGCTTCGGTAGCGAGTGGTTCTGGTGGTATTGGCAAAAGGAAA
 AGATACCGAAGTATGTGGAATTTATGAAAGATAATTACCCTCCTAGTTTCAAATATGAAGAT
 TTTGGACCACTATTTACAGCAAATTTTTTAATGCCAACAGTGGGCAGATATTTTTCAGGC
 CTCTGGTGCCAATACATTGTCTTAACTTCCAACATCATGAAGGCTTTACCTTGTGGGGT
 CAGAATATTCGTGGAACTGGAAATGCCATAGATGAGGGGCCAAGAGGGACATTGTCAAGGAA
 CTTGAGGTAGCCATTAGGAAACAGAACTGACCTGCGCTTTTGAGCTGTACTATTCCCTTTTTGA
 ATGTTTTTCATCCGCTCTCTCTTGAGGATGAATCCAGTTTATTCCATAAGCGGCAATTTCCAG
 TTTCTAAGACATTGCCAGAGCTCTATGAGTTAGTGAACAACTATCAGCCTGAGGTTCTGTGG
 TCGGATGGTGACGGAGGAGCACCGGATCAATACTGGAACAGCACAGGCTTCTTGGCCTGGTT
 ATATAATGAAAGCCCAGTTCCGGGGCAAGTAGTCACCAATGATCGTTGGGGAGCTGGTAGCA
 TCTGTAAGCATGGTGGCTTCTATACCTGCAGTGATCGTTATAACCCAGGACATCTTTTGCCA
 CATAAATGGGAAAATGCAATGACAATAGACAACTGTCTCTGGGGCTATAGGAGGGAAGCTGG
 AATCTCTGACTATCTTACAATTGAAGAATTGGTGAAGCAACTGTAGAGACAGTTTCATGTG
 GAGGAAATCTTTTGATGAATATTGGGCCCACTAGATGGCACCATTCTGTAGTTTTTGAG
 GAGCGACTGAGGCAAGTGGGGTCTCTGGCTAAAAGTCAATGGAGAAGCTATTTATGAAACCTA
 TACCTGGCGATCCAGAAATGACACTGTCACCCAGATGTGTGTACACATCCAAGCCTAAAG
 AAAAAATTAGTCTATGCCATTTTCTTAAATGGCCACATCAGGACAGCTGTTCTTGGCCAT
 CCCAAAGCTATTCTGGGGGCAACAGAGGTGAAACTACTGGGCCATGGACAGCCACTTAACTG
 GATTTCTTTGGAGCAAAATGGCATTATGGTGAAGTGCACAGCTAACCATTCATCAGATGC
 CGTGTAATGGGGCTGGGCTCTAGCCCTAACTAATGTGATCTAAAGTGCAGCAGAGTGGCTG
 ATGCTGCAAGTTATGTCTAAGGCTAGGAACTATCAGGTGTCTATAATTGTAGCACATGGAGA
 AAGCAATGTAACTGGATAAGAAAATTATTTGGCAGTTTCAGCCCTTTCCCTTTTTCCCCTA
 AATTTTTCTTAAATTACCATGTAAACATTTTAACTCTCCAGTGCACTTTGGCATTAAAGTC
 TCTTCACATTGATTGTTTCCATGTGTGACTCAGAGGTTGAGAATTTTTTTCACATTATAGTAG
 CAAGGAATGGTGGTATTATGGACCGAACTGAAAATTTTATGTGGAAGCCATATCCCCCATG
 ATTATATAGTTATGCATCACTTAATATGGGGATATTTCTGGGAAATGCATTGCTAGTCAAT
 TTTTTTTGTGCCAACATCATAGAGTGATTTACAAAATCCTAGATGGCATAGCCTACTACA
 CACCTAATGTGTATGGTATAGACTGTTGCTCCTAGGCTACAGACATATACAGCATGTTTACTG
 AATACTGTAGGCAATAGTAACAGTGGTATTTGTATATCGAAACATATGAAACATAGAGAAG
 GTACAGTAAAAATACTGTAAATAAAATGGTGCACCTGTATAGGGCACTTACCACGAATGGAG
 CTTACAGGACTGGAAGTTGCTCTGGGTGAGTCAGTGAGTGAATGTGAAGGCTGAGACATT
 TTGAACACTGCCAGACGTTATAAAATCTGTATGCTTAGGCTACACTACATTATATAAAAAAA
 GTTTTTCTTCTTCAATTATAAATAACATAAGTGTACTGTAACCTTACAAACGTTTTTAATT
 TTTAAACCTTTTGGTCTTTTGTATAACACTTAGCTTAAACATAAACTCATGTGCA
 ATGTAA

09904533 071301

FIGURE 72

MRPQELPRLAFPLLLLLLLLLLLLLPPPPCPAHSATRFDPWTESLDARQLPAWFDQAKFGIFIHWG
VFSVPSFGSEWFWWYQKEKIPKYVEFMKDNYPSPSKYEDFGPLFTAKFFNANQWADIFQAS
GAKYIIVLTSKHHEGFTLWGSEYSWNWNAIDEGPKRDIVKELEVAIRNRTDLRFGLYYSLFEW
FHPLFLEDESSSFHKRQFPVSKTLPPELYELVNNYQPEVLWSDGDDGAPDQYWNSTGFLAWLY
NESPVRGTVVTNDRWGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDKLSWGYRREAGI
SDYLTIELVKQLVETVSCGGNLLMNIGPTLDGTISVVFEERLRQVGSWLKVNGEAIYETYT
WRSQNDTIVTPDVWYTSKPKKEKLVYAIFLKWPTSGQLFLGHGPKAILGATEVKLLGHGQPLNWI
SLEQNGIMVELPQLTIHQMPCKWGWALALTNVI

Signal sequence:

amino acids 1-28

N-glycosylation site.

amino acids 171-175, 239-243, 377-381

Casein kinase II phosphorylation site.

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319,
375-375

Tyrosine kinase phosphorylation site.

amino acids 361-369, 389-397

N-myristoylation site.

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

Leucine zipper pattern.

amino acids 410-432

Alpha-L-fucosidase putative active site.

amino acids 283-295

00904833-07201

FIGURE 73

AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATAGT
TCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGCCATC
TGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCACTGCTGGTGTG
CTTCTCACTTCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAAAGAGCT
TTCCATCCAGGTGTCAATGCAGAAATATGGGGATCACCTTGTGAGCAAAAAGGCGAACCCAG
AGCTGAATTTACAGAAAGCTAAGGAGGCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAG
GACCAAGTTGAAACAGCCTTGAAGCTAGCTTTGAAACTTGACAGCTATGGCTGGGTTGGAGA
TGGATTCTGGTCTATCTAGGATTAGCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTG
TCCTGATTTGGAAGGTTCCAGTGAGCCGACAGTTTGAGCCTATTGTTTACAACTCATCTGAT
ACTTGAGCTAACTCGTGCAATTCAGAAATATCACCACCAAGATCCCATATTCAACACTCA
AAGTGCACACAAACAACAGAATTTATTGTCAGTGACAGTACCTACTCGGTGGCATCCCCTT
ACTCTACAATACCTGCCCTACTACTACTCTCTCTGCTCCAGCTTCCACTTCTATTCCACGG
AGAAAAAATTTGATTTGTGTACAGAAAGTTTTATGGAACCTAGCACCATTGTCTACAGAAAC
TGAACCATTTGTTGAAAATAAAGCAGCAATCAAGAATGAAGCTGTGGGTTGGAGGTGTCC
CCACGGCTCTGCTAGTGCTGTCTCTCTCTCTTGTGTGTGACAGTGGTCTTGGATTTTGCT
TATGTCAAAGGTATGTGAAGGCCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGAT
CGAAACCAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCTTAATGAGGAATCAAAGA
AAACTGATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAACTACCGTGCATGCCCTGGAA
GCTGAAGTTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTTCTTTCATGCTCC
TTACCTTGCCCCAGCTGGGAAATCAAAGGGCCAAAGAACCAAAGAAGAAAGTCCACCTT
GGTTCTTAAGTGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAAATGC
CCTTCTCCTTATTGTAAACCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCCACGGCC
TTTCTAGCCTGGCTATGTCTTAATAATATCCCACTGGGAGAAAGGAGTTTGTCAAAGTGCAA
GGACCTAAAACATCTCATCAGTATCCAGTGGTAAAAAGGCCCTCTGGCTGTCTGAGGCTAGG
TGGGTTGAAAGCCAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCCGACAGCTCAGAC
CCTTTCTTCAAGCTCTGAAAGAGAAACACGATATCCCACTGACATGTCTTCTGAGCCCGGTA
AGAGCAAAAGAAATGGCAGAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCATAAATTGAG
ACCTAATCTCTGTAAGCTAAAATAAAGAAATAGAACAAGGCTGAGGATACGACAGTACACT
GTCAGCAGGAGTGTAAACACAGACAGGGTCAAAGTGTCTTCTGTGAACACATTGAGTTGGA
ATCACTGTTTTAGAACACACACACTTACTTTTTCTGGTCTCTACCACTGCTGATATTTCTCT
AGGAAATATACTTTTACAAGTAACAAAAATAAAAACTCTTAATAATTTCTATTTTATCTGA
GTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTAAAAAGTAATAAAATTC
ACAAACATTGTGCTGAATAGCTACTATATGTCAAGTGCTGTGCAAGGTATTACACTCTGTAAT
TGAATATTATCTCCTCAAAAAATTCACATAGTAGAACGCTATCTGGGAAGCTATTTTCTCA
GTTTTGATATTTCTAGCTTATCTACTTCCAACTAAATTTTATTTTGTGAGACTAATCTT
ATTCAATTTCTCTAATATGGCAACCATTAACCTTAATTTATTATTAAACATACCTAAGAG
TACATTGTTACCTCTATATACCAAGCACATTTTAAAAAGTGCCATTACAAATGTATCACTA
GCCCTCCTTTTCCAAACAAGAGGAGCTGAGAGATGAGAAATATTGTGACAAAAAATTA
AGCATTTAGAAAACTT

FIGURE 74

MARCFSLVLLLTISIWTRLLVQGSRLAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACR
LLGLSLAGKDQVETALKASFETCSYGWVGDFVVISRISPNPKCGKNGVGVLWKVPVSRQF
AAYCYNSSDTWTNSCIPEIIITKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTPP
APASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAFKNEAAGFGGVPTALLVLALLFF
GAAAGLGFCYVKRYVKAFFFTNKNQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSP
SKTTVRCLAEAV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 53-57, 130-134, 289-293

Casein kinase II phosphorylation site.

amino acids 145-149, 214-218

Tyrosine kinase phosphorylation site.

amino acids 79-88

N-myristoylation site.

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

FIGURE 75

AGATGCGGTCTTGGCACCTCTAATTGCTCTCGTGATTTCGGTGCCGCGACTTTCACGATGG
CTCGCCCAACCTTACTACCTTCTGTGCGCCCTGCTCTCTGCTGCCTTCTACTCTGTGAGGAA
ACTGCCCGCGTCTGCCACGCTCTGCCACCCCAACGCGAAGACGGTAACCCGTGTGACTTTG
ACTGGAGAGAAAGTGGAGATCCTGATGTTTCTCAGTGCCATTGTGATGATGAAGAACCGCAGA
TCCATCACTGTGGAGCAACATATAGGCAACATTTTCATGTTTAGTAAAGTGGCCAAACAAT
TCTTTTCTTCCGCTTGGATATTGCGATGGGCTACTTTACATCACACTCTGCATAGTGTTC
TGATGACGTGCAACCCCCCTATATATGGGCCCTGAGTATATCAAGTACTTCAATGATAAA
ACCATTGATGAGGAAGTAGAACGGGACAAGAGGGTCACTTGGATTGTGGAGTTCCTTTGCCAA
TTGGTCTAATGACTGCCAATCATTTGCCCTATCTATGCTGACCTCTCCCTTAAATACAAC
GTACAGGGCTAAATTTTGGGAAGGTGGATGTTGGACGCTATACTGATGTTAGTACGCGGTAC
AAAGTGAGCACATCACCCCTCACCAAGCAACTCCCTACCCTGATCCTGTTCCAAGGTGGCAA
GGAGGCAATGCGCGGCCACAGATTGACAAGAAAGGACGGGCTGTCTCATGGACCTTCTCTG
AGGAGAATGTGATCCGAGAATTTAACTTAAATGAGCTATACCAGCGGGCCAAAGAACTATCA
AAGGCTGGAGACAATATCCCTGAGGAGCAGCCTGTGGCTTCAACCCCAACACAGTGTGAGA
TGGGGAAAACAAGAAGGATAAATAAGATCCTCACTTTGGCAGTGCTTCCTCTCTGTCAATT
CCAGGCTCTTTCCATAACCACAAGCCTGAGGCTGCAGCCTTNNATTNATGTTTTCCCTTTGG
CTNGACTGGNTGGGGCAGCATGCAGCTTCTGATTTTAAAGAGGCATCTAGGGAATTGTCAG
GCACCCTACAGGAAGGCCTGCCATGCTGTGGCCAACCTGTTTCACTGGAGCAAGAAAGAGATC
TCATAGGACGGAGGGGAAATGGTTTCCCTCCAAGCTTGGGTGAGTGTGTTAACTGCTTATC
AGCTATTCAGACATCTCCATGGTTTCTCCATGAAACTCTGTGGTTTCATCATTCCTTCTTAG
TTGACCTGCACAGCTTGTTAGACCTAGATTAAACCTAAGGTAAGATGCTGGGGTATAGAA
CGCTAAGAATTTCCCCAAGGACTCTTGCTTCCTTAAGCCCTTCTGGCTTCGTTTATGGTC
TTCATTAAAGTATAAGCCTAACTTTGTGCTAGTCCTAAGGAGAAACCTTTAACCACAAG
TTTTTATCATTGAAGACAATATTGAACAACCCCTATTTTGTGGGGATTGAGAAGGGGTGAA
TAGAGGCTTGAGACTTTCCTTTGTGTGGTAGGACTTGGAGGAGAAATCCCCTGGACTTTCAC
TAACCCCTGACATACTCCCCACCCAGTTGATGGCTTCCGTAATAAAAAGATTGGGATT
TCCTTTTG

FIGURE 76

MAVLAPLIALVYSVPRLSRWLAQPYLLSALLSAAFLLVRLPPLCHGLPTQREDGNPCDFD
WREVEILMFLSAIVMMKNRRSITVEQHIGNIFMFSKVANTILFFRLDIRMGLLYITLCIVFL
MTCKPPLYMGPEYIKYFNDKTIDEELERDKRVTWIVEFFANWSNDCQSFAPIYADLSLKYN
TGLNFGKVDVGRYTDVSTRYKVSTSPLTKQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSE
ENVIREFNLNELYQRAKKLSKAGDNIPEEQPVASTPTTVSDGENKKDK

Signal sequence:

amino acids 1-48

Transmembrane domain:

amino acids 111-125

N-glycosylation site.

amino acids 165-169, 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 154-158, 265-269

Casein kinase II phosphorylation site.

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

N-myristoylation site.

amino acids 188-194, 225-231

Myb DNA-binding domain repeat signature 1.

amino acids 244-253

Case	Age	Sex	Duration	Location	Outcome
1	10	M	10 days	USA	Recovered
2	12	F	15 days	USA	Recovered
3	15	M	20 days	USA	Recovered
4	18	F	25 days	USA	Recovered
5	20	M	30 days	USA	Recovered
6	22	F	35 days	USA	Recovered
7	25	M	40 days	USA	Recovered
8	28	F	45 days	USA	Recovered
9	30	M	50 days	USA	Recovered
10	32	F	55 days	USA	Recovered
11	35	M	60 days	USA	Recovered
12	38	F	65 days	USA	Recovered
13	40	M	70 days	USA	Recovered
14	42	F	75 days	USA	Recovered
15	45	M	80 days	USA	Recovered
16	48	F	85 days	USA	Recovered
17	50	M	90 days	USA	Recovered
18	52	F	95 days	USA	Recovered
19	55	M	100 days	USA	Recovered
20	58	F	105 days	USA	Recovered
21	60	M	110 days	USA	Recovered
22	62	F	115 days	USA	Recovered
23	65	M	120 days	USA	Recovered
24	68	F	125 days	USA	Recovered
25	70	M	130 days	USA	Recovered
26	72	F	135 days	USA	Recovered
27	75	M	140 days	USA	Recovered
28	78	F	145 days	USA	Recovered
29	80	M	150 days	USA	Recovered
30	82	F	155 days	USA	Recovered
31	85	M	160 days	USA	Recovered
32	88	F	165 days	USA	Recovered
33	90	M	170 days	USA	Recovered
34	92	F	175 days	USA	Recovered
35	95	M	180 days	USA	Recovered
36	98	F	185 days	USA	Recovered
37	100	M	190 days	USA	Recovered
38	102	F	195 days	USA	Recovered
39	105	M	200 days	USA	Recovered
40	108	F	205 days	USA	Recovered
41	110	M	210 days	USA	Recovered
42	112	F	215 days	USA	Recovered
43	115	M	220 days	USA	Recovered
44	118	F	225 days	USA	Recovered
45	120	M	230 days	USA	Recovered
46	122	F	235 days	USA	Recovered
47	125	M	240 days	USA	Recovered
48	128	F	245 days	USA	Recovered
49	130	M	250 days	USA	Recovered
50	132	F	255 days	USA	Recovered
51	135	M	260 days	USA	Recovered
52	138	F	265 days	USA	Recovered
53	140	M	270 days	USA	Recovered
54	142	F	275 days	USA	Recovered
55	145	M	280 days	USA	Recovered
56	148	F	285 days	USA	Recovered
57	150	M	290 days	USA	Recovered
58	152	F	295 days	USA	Recovered
59	155	M	300 days	USA	Recovered
60	158	F	305 days	USA	Recovered
61	160	M	310 days	USA	Recovered
62	162	F	315 days	USA	Recovered
63	165	M	320 days	USA	Recovered
64	168	F	325 days	USA	Recovered
65	170	M	330 days	USA	Recovered
66	172	F	335 days	USA	Recovered
67	175	M	340 days	USA	Recovered
68	178	F	345 days	USA	Recovered
69	180	M	350 days	USA	Recovered
70	182	F	355 days	USA	Recovered
71	185	M	360 days	USA	Recovered
72	188	F	365 days	USA	Recovered
73	190	M	370 days	USA	Recovered
74	192	F	375 days	USA	Recovered
75	195	M	380 days	USA	Recovered
76	198	F	385 days	USA	

FIGURE 78

MGLLLLVLPLLLPGSYGLPFYNGFYYSNSANDQNLGNHGKDLLNGVKLVVETPEETLFTYQ
GASVILPCRYRYEPALVSPRRVRVKKWKLSENGAPEKDLVAIGLRHRSFGDYQGRVHLRQD
KEHDVSLLEIQDLRLLEDYGRYRCEVIDGLEDESGLVELELRGVVFPYQSPNGRYQFNFHEGQQ
VCAEQAAVVASFEQLFRAWEEGLDWCNAGWLQDATVQYPIMLPRQPCGGPGLAPGVRSYGPR
HRRLLHRYDVFCFATALKGRVYYLEHPEKLTLTAREACQEDDATIAKVGQLFAAWKFFHGLDR
CDAGWLADGSVRYFPVVHPHPNCGPPEPGVRSFGFPDPQSRLYGVYCYRQH

Signal sequence:

amino acids 1-17

Casein kinase II phosphorylation site.

amino acids 29-33, 53-57, 111-115, 278-282

Tyrosine kinase phosphorylation site.

amino acids 137-145

N-myristoylation site.

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313

FIGURE 79

GGAGAGCGGAGCGAAGCTGGATAAACAGGGGACCGATGATGTGGCGACCATCAGTTCGTGCTGC
TTCTGTTGCTACTGAGGCACGGGGCCAGGGGAAGCCATCCCCAGACGCAGGCCCTCATGGC
CAGGGGAGGGTGACACAGGCGGGCCCCCTGAGCGACGCTCCCCATGATGACGCCACAGGGAA
CTTCCAGTACGACCATGAGGCTTTCCTGGGACGGGAAGTGGCCAAGGAATTCGACCAACTCA
CCCCAGAGGAAAGCCAGGCCCGTCTGGGGCGGATCGTGGACCGCATGGACCGCGCGGGGGAC
GGCGACGGCTGGGTGTCTGCTGGCCGAGCTTCGCGCGTGGATCGCGCACACGCAGCAGCGGCA
CATACGGGACTCGGTGAGCGCGGCCTGGGACACGTACGACACGGACCGCGACGGGCGTGTGG
GTTGGGAGGAGCTGCGCAACGCCACCTATGGCCACTACGCGCCCGGTGAAGAAATTCATGAC
GTGGAGGATGCAGAGACCTACAAAAAGATGCTGGCTCGGGACGAGCGGCGTTTCCGGGTGGC
CGACCAGGATGGGGACTCGATGGCCACTCGAGAGGAGCTGACAGCCTTCCTGCACCCCGAGG
AGTTCCTCACAATGCGGGACATCGTGATTGCTGAAACCTGGAGGACCTGGACAGAAACAAA
GATGGCTATGTCCAGGTGGAGGAGTACATCGCGGATCTGTACTCAGCCGAGCCTGGGGAGGA
GGAGCCGGCGTGGGTGCAGACGGAGAGGCAGCAGTTCGCGGACTTCGCGGATCTGAACAAGG
ATGGGCACCTGGATGGGAGTGAGGTGGGCCACTGGGTGCTGCCCCCTGCCAGGACCAGCCC
CTGGTGGAAGCCAACCACTGTCTGCACGAGAGCGACACGGACAAGGATGGCGGCTGAGCAA
AGCGGAAATCTGGGTAATTGAACATGTTTGTGGGCAGTCAGGCCACCAACTATGGCGAGG
ACCTGACCCGGCACCACGATGAGCTGTGAGCACCGCGCACCTGCCACAGCCTCAGAGGCCCG
CACAATGACCCGGAGAGGGGGCCGCTGTGGTCTGGCCCCCTCCTGTCCAGGCCCGCAGGAG
GCAGATGCAGTCCCAGGCATCCTCCTGCCCCCTGGGCTCTCAGGACCCCTGGGTGCGCTTC
TGTCCTGTACACCCCCAACCCAGGGAGGGGCTGTCTATAGTCCCAGAGGATAAGCAATAC
CTATTTCTGACTGAGTCTCCAGCCCAGACCCAGGGACCCTTGGCCCCAAGCTCAGCTCTAA
GAACCGCCCCAACCCCTCCAGCTCCAAATCTGAGCCTCCACCACATAGACTGAAACTCCCTT
GGCCCCAGCCCTCTCTGCTGGCCTGGCCTGGGACACCTCCTCTCTGCCAGGAGGCAATAA
AAGCCAGCGCCGGGACCTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAA

FIGURE 80

MMWRPSVLLLLLLLRHGAQGKPSPDAGPHGQGRVHQAAFLSDAPHDDAHGNFQYDHEAFLGR
EVAKFPDQLTFEESQARLGRIVDRMDRAGDGDGWSLAELEAWIAHTQQRHIRDSVSAAWDT
YDTRDRGRVGWEELRNATYGHYAPGEEFHDVEDAETYKKMLARDERRFRVADQDGDSMATRE
ELTAFLHPEEFPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEEPAWVQTERQQ
FRDFRDLNKGHLGDSEVGHWWLPPAQDQPLVEANHLLHESDTDKDGRLSKAEILGNWNMFV
GSQATNYGEDLTRHHDEL

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 140-144

Casein kinase II phosphorylation site.

amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,
291-295, 298-302

N-myristoylation site.

amino acids 263-269, 311-317

Endoplasmic reticulum targeting sequence.

amino acids 325-330

FIGURE 81

GGGGCCCTTGCCCTCCGCACTCGGGCGCAGCCGGGTGGATCTCGAGCAGGTGCGGAGCCCCGG
 GCGGCGGGCGCGGGTGCGAGGGATCCCTGACGCCCTCTGTCCCTGTTTCTTTGTGCGCTCCAG
 CTGTCTGTGTCGTGTTTTGGCGCCCCGCCCTCCCGCGGTGCGGGGTGCAACCGGATCCTG
 GGCTTCGCTCGATTTCGCCGCCAGGCGCCCTCCAGACCTAGAGGGGCGCTGGCCCTGGAGCAG
 CGGGTCGTCTGTGTCCTCTCTCTCTGCGCCGCGCCCCGGGGATCCGAAGGGTGCGGGGCTCT
 GAGGAGGTGACGCGCGGGGCCCTCCCGCACCTGGCCTTGCCCGCATTCTCCCTCTCTCCAG
 GTGTGAGCAGCCTATCAGTCACCAATGTCGCCGAGCCTGGATCCCGGCTCTCGGCCCTCGGTGTG
 TGTCTGCTGCTGCTGCGCGGGGCCCGCGGGCAGCGAGGGAGCCGCTCCCATTGCTATCACATG
 TTTTACAGAGGCTTGGACATCAGGAAAGAGAAAGCAGATGTCTCTGCCCAGGGGGCTGCC
 CTCTTGAGGAATTCTCTGTGTATGGGAACATAGTATATGCTTCTGTATCGAGCATATGTGGG
 GCTGCTGTCCACAGGGGAGTAATCAGCAACTCAGGGGGACCTGTACGAGCTATAGCCCTACC
 TGGTCGAGAAAACTATTCTCAGTAGATGCCAATGGCATCCAGTCTCAAAATGCTTTCTAGAT
 GGTCTGCTCTTTTACAGTAACATAAGGCAAAAGTAGTACACAGGAGGCCACAGGACAAGCA
 GTGTCCACAGCACATCCACCAACAGGTAAACGACTAAAGAAAAACCCCGAGAAGAAAACTGG
 CAATAAAGATTGTAAAGCAGACATTGCATTCTTGATTGATGGAAGCTTTAATATTGGGCAGC
 GCCGATTTAATTTACAGAAGAAATTTTGTGGAAAAAGTGGCTCTAATGTTGGGAATTGGAACA
 GAAGGACCAATGTGGGCTTTGTTCAAGCCAGTGAACATCCCAAAATAGAATTTTACTTGAA
 AAATCTTACATCAGCCAAGAGATGTTTTGTTTGGCCATAAAGGAAGTAGGTTTTCAGAGGGGGTA
 ATTCCTCAATACAGGAAAAGCCTTGAAGCATACTGCTCAGAAATCTTTCACGGTAGATGCTGGA
 GTAAGAAAAGGGATCCCCAAAGTGGTGGTGGTATTATTATGATGGTTGGCCCTTCTGATGACAT
 CGAGGAAGCAGGCATTGTGGCCAGAGAGTTTGGTGTCAATGTATTTATAGTTTCTGTGGCCA
 AGCCTATCCCTGAAGAACTGGGGATGGTTCAGGATGTACATTGTTGACAAGGCTGTCTGT
 CGGAATAATGGCTTCTCTCTTACCACATGCCCAACTGGTTTGGCACCAAAAACTAGTAAA
 GCCTCTGGTAGCAAGCTGTGCACTCATGAACAAATGTGTGACAGCAAGACTGTTATCAATACT
 CAGTGAACATTGCGCTTTCTAATTGATGGCTCCAGCAGTGTGGAGATAGCAATTTCCGCTC
 ATGCTTGAATTTGTTTCCAACTAGCCAAGACTTTTGAATCTCGGACATTGGTGCCAAGAT
 AGCTGCTGTACAGTTTACTTTATGATCAGCGCACGGAGTTCAGTTTCACTGACTATAGCACCA
 AAGAGAATGTCCTAGCTGTCTATCAGAAACATCCGCTATATGAGTGGTGAACAGCTACTGGT
 GATGCCATTTCTTCACTGTTAGAAAATGTGTTTGGCCCTATAAGGGAGAGCCCCAACAGAA
 CTTCTTAGTAATTTGTCAAGATGGGCAGTCTCATGATGATGTTCAAGGCCCTGCAGCTGTG
 CACATGATGAGGAATCACTATCTTCTCTGTTGGTGTGGCTTGGGCACCTCTGGATGACCTG
 AAAGATATGGCTTTCTAAACCGAAGGAGTCTCAGCTTTCTTCAAGAGAGTTTACAGGATT
 AGAACCAATTGTTTCTGATGTCTATCAGAGGCATTGTAGAGATTTCTTAGAATCCAGCAAT
 AATGGTAACATTTTACAACTGAAAGAAAAAGTACAAGGGGATCCAGTGTGTAATTTGATT
 CTCATAATACTGAATGCTTTAGCATACTAGAATCAGATACAAAATATTAAAGTATGTCAAC
 AGCCATTTTAGGCAATAAGCACTCCTTTAAAGCCGCTGCCTTCTGGTTACAAATTTACAGTGT
 ACTTTGTTAAAAACACTGCTGAGGCTTCATAATCATGGCTCTTAGAAACTCAGGAAAGAGGA
 GATAATGTGATTAAAAACCTTAAGAGTTTCAACCATGCCCTACTAAATGTACAGATATGCAAA
 TTCCATAGCTCAATAAAAGAACTGTGATCTTAGACCAAAAAAAAAA

FIGURE 82

MSAAWIPALGLGVCLLLLPGPAGSEGAAPIAITCFTRGLDIRKEKADVLCPPGGCPLEEFVY
GNIVYASVSSICGAAVHRGVISNSGGFVRVYSLPGRENYSSVDANGIQSQMLSRWSASFTVT
KGKSSTQEATGQAVSTAHPPTGKRLKKTPEKKTGNKDKADIAFLIDGSFNIGQRRFNLQKN
FVGKVALMLGIGTEGPHVGLVQASEHPKIEFYLNFTSAKDVLFAlKEVGFRGGNSNTGKAL
KHTAQKFFTVDAGVRKGIPKVVVVFIDGWPSDDIEEAGIVAREFGVNVFIVSVAKPIPEELG
MVQDVTfVDKAVCRNNGFFSYHMPNWFGTtKYVKPLVQKLCtHEQMMSKTCYNSVNIaFLI
DGSSSVGDSNFRMLLEFVSNIAKTfEISDIGAKIAAVQfTYDQrTEfSfTDYSTKENVLAVI
RNIRYMSGGTATGDAISfTVRNfVFGPIRESfPNKfNfLVITDGQSYDDVQGPAAAAHDAGITI
FSVGVAWAPLDDLKDMASKPKESHAFfTfREfTGLEPIVSDVIRGICRDFLESQQ

Signal sequence:

amino acids 1-24

N-glycosylation site.

amino acids 100-104, 221-225

Casein kinase II phosphorylation site.

amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,
425-429, 478-482, 528-532

N-myristoylation site.

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

Amidation site.

amino acids 145-149

FIGURE 84

MQRLGATLLCLLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEEATLNEMFREVEELMEDTQ
HKLRS AVEEMEAEAAAAKASSEVNLANLPPSYHNETNTDTKVGNNTIHVHREIHKITNNQTG
QMVFSETVITSVGDEEGRRSHECIIDEDCGFSMYCQFASFQYTCQPCRGQRMMLCTRDSECCG
DQLCVWGHCTKMATRGSGNTICDNQRDCQPGLCCAFQRGLLFPVCTPLPVEGELCHDPASRL
LDLITWELEPDGALDRCPASGLLCQPHSHSLVYVCKPTFVGSRDQDGEILLPREVPDEYEV
GSFMEEVRQELEDLERSLTEEMALGEPAAAAAALLGGEET

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 96-100, 106-110, 121-125, 204-208

Casein kinase II phosphorylation site.

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,
327-331

N-myristoylation site.

amino acids 202-208, 217-223

Amidation site.

amino acids 140-144

FIGURE 86

MRLLVAPLLLLAWVAGATATVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDCNDLFLTA
VPPALPAGTQTLTLLQSNISIVRVQSELGYLANLTELDLSQNSFSDARDCDFHALPQLLSLHL
EENQLTRLEDHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLNSNLLRAIDSRWFE
MLPNLEILMIGGNKVDAIILDMNFRPLANLRSVLGAMNLRREISDYALEGLQSLESLSFYDNQ
LARVPRRALEQVPGPKFLDLNKNPLQRVGPGDFANMLHLKELGLNNMEELVSIDKFALVNLFP
ELTKLDITNNPRLSFIHPRAFHHLPMETLMLNNAALSALHQQTVESLPNLQEVGLHGNIIR
CDCVIRWANATGTRVRVFIIEPOSTLCAEPPDLQRLPVREVPPFREMTDHCLPLISPRSFPFSLQ
VASGESMVLHCRALAEPEPEIYWVTPAGLRLLTPAHAGRRYRVYPEGTELELRVTAEEAGLYT
CVAQNVLGADTKTVSVVVGRALLQPGRDEGQGLELRVQETHPYHILLSSWVTPPNTVSTNLTW
SSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLQVAFADAHTQLACVWARTKEATS
CHRALGDRPGLIAILALAVLLLAAGLAAHLGTGQPRKGVGGRRPLPPAWAFWGSAPSVRV
SAPLVLPWNPGRKLPSSSEGETLLPPLSQNS

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 629-648

N-glycosylation site.

amino acids 94-98, 381-385, 555-559, 583-587

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 485-489

Casein kinase II phosphorylation site.

amino acids 46-50, 51-55, 96-100, 104-108, 130-134, 142-146,
243-247, 313-317, 488-492, 700-704

Tyrosine kinase phosphorylation site.

amino acids 532-540

N-myristoylation site.

amino acids 15-21, 493-499, 566-572

Amidation site.

amino acids 470-474, 660-664, 692-696

FIGURE 88

MRQTIKVIKFIILICYTVYYVHNKFDVDCTVDIESLTGYRTYRCAHPLATLTKILASFYI
SLVIFYGLICMYTLWWMRLRRSLKKYSFESIREESSYSDIPDVKNDFAFMLHLIDQYDPLYSK
RFAVFLSEVSENKLRQLNLNNEWTLDKLRQLTKNAQDKLELHFLMLSGIPDTVFDLVELEV
LKLELIPDVTIPPSIAQLTGLKELWLYHTAAKIEAPALAFLRENLRALHIKFTDIKEIPLWI
YSLKLTLEELHLTGNLSAENNRYIVIDGLRELKRLKVLRLKSNLSKLPQVVTDVGVHLQKLSI
NNEGTKLIVLNSLKMANLLELELIRCDLERIPHSIFSLHNLQEIDLKDNNLKTIIEEIIISFQ
HLHRLTCLKLWYNHIAIYIPIQIGNLTNLERLYLNRNKIEKIPTQLFYCRKLRYLDLSHNNLT
FLPADIGLLQNQLNLAITANRIETLPELFPQCRKLRAHLGNNVLQSLPSRVGELTNLTQIE
LRGNRLECLFVELGECPLLKRSGLVVEEDLFNTLPPEVKERLWRADKEQA

Transmembrane domain:

amino acids 51-75 (type II)

N-glycosylation site.

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 85-89

Casein kinase II phosphorylation site.

amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,
398-402, 493-497

N-myristoylation site.

amino acids 173-179, 261-267, 395-401, 441-447

FIGURE 90

MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATNSC
KNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSDLKPRKTTWLQAASLLFVDNPNVGTGFSY
VNGSGAYAKDLAMVASDMMVLLKTTFFSCHKEFQTVFFYIFSESYGGKMAAGIGLELYKAIQR
GTIKCNFAGVALGDSWISFVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNAVNGGLYRE
ATELWGKAEMIIIEQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRHVRHLQRDALS
QLMNGPIRKKLKIIPEDQSWGQATNVFVNMEEDFMKPVISIVDELLEAGINVTYVNGQLDL
IVDTMGQEAWRKLLKWPELPKFSQLKWKALYSDPKSLETSFAFVKSYNLAFYWILKAGHMVP
SDQGDMALKMMRLVTQQE

Signal sequence:

amino acids 1-25

N-glycosylation site.

amino acids 64-68, 126-130, 362-366

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 101-105

Casein kinase II phosphorylation site.

amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

N-myristoylation site.

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,
187-193, 195-201, 331-337, 332-338, 360-366

FIGURE 91

GGCCGCGGGAGAGGAGGCCATGGGCGCGCGCGGGCGCTGCTGCTGGCGCTGCTGCTGGCTC
GGGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCGCGCCGTTATCAGGACCATGCGGCCGA
CGGGTCATCACGTCGCGCATCGTGGGTGGAGAGGACGCCGAACTCGGGCGTTGGCCGTGGCA
GGGGAGCCTGCGCCTGTGGGATTCCCACGTATGCGGAGTGAGCCTGCTCAGCCACCGCTGGG
CACTCACGGCGGCGCACTGCTTTGAAACCTATAGTGACCTTAGTGATCCCTCCGGGTGGATG
GTCCAGTTTGGCCAGCTGACTTCCATGCCATCCTTCTGGAGCCTGCAGGCCTACTACACCCG
TTACTTCGTATCGAATATCTATCTGAGCCCTCGCTACCTGGGGAATTCACCCATGACATTG
CCTTGGTGAAGCTGTCTGCACCTGTGCACCTACACTAAACACATCCAGCCCATCTGTCTCCAG
GCCTCCACATTTGAGTTTGAGAACCGGACAGACTGCTGGGTGACTGGCTGGGGGTACATCAA
AGAGGATGAGGCACTGCCATCTCCCCACACCCTCCAGGAAGTTCAGGTCGCCATCATAAACA
ACTCTATGTGCAACCACCTCTTCTCAAGTACAGTTTCCGCAAGGACATCTTTGGAGACATG
GTTTGTGCTGGCAACGCCCAAGGCGGAAGGATGCCTGCTTCGGTGACTCAGGTGGACCCTT
GGCCTGTAAACAAGAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGGAGTGGGCTGTG
GTCGGCCCAATCGGCCCGGTGTCTACACCAATATCAGCCACCCTTTGAGTGGATCCAGAAG
CTGATGGCCCAGAGTGGCATGTCCCAGCCAGACCCTCCTGGCCACTACTCTTTTTCCCTCT
TCTCTGGGCTCTCCCACTCCTGGGGCCGGTCTTGAGCCCTACCTGAGCCCATGCAGCCTGGGGC
CACTGCCAAGTCAGGCCCTGGTTCTCTTCTGTCTTGTGTTGGTAATAAACACATTCCAGTTGA
TGCCTTGCAGGGCATTCTTCAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 92

MGARGALLLALLLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSRLRW
DSHVCVGSLLSHRWALTAAHCFETYSDLSDPSGWMVQFGQLTSMPSFWSLQAYYTRYFVSNI
YLSPRYLGNSPYDIALVKLSAPVTTYTKHIQPICLQASTFEFENRTDCWVTGWGYIKEDEALP
SPHTLQEVQVAIINNSMCNHLFLKYSFRKDI FGDMVCAGNAQGGKDACFGDSGGPLACNKNG
LWYQIGVVSWGVGGRPNRPGVYTINISHHFEWIQKLMAQSGMSQPDPSWPLLFFPLLWALPL
LGPV

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 167-171, 200-204, 273-277

Casein kinase II phosphorylation site.

amino acids 86-90, 134-138, 161-165, 190-194, 291-295

N-myristoylation site.

amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245,
259-265, 269-275

Amidation site.

amino acids 33-37

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 252-263,

Serine proteases, trypsin family, histidine active site.

amino acids 78-84

FIGURE 93

CCCACGCGTCCGCGGACGCGTGGGAAGGGCAGAAATGGGACTCCAAGCCTGCCTCCTAGGGCT
 CTTTGGCCCTCATCTCTCTGGCAAAATGCAGTTACAGCCCGGAGCCCGACAGCGGGAGBACGC
 TGCCCCCAGGCTGGGTGTCCCTGGGCCGTGCGGACCCTGAGGAAGAGCTGAGTCTCACTTT
 GCCCTGAGACAGCAGAATGTGGAAAGACTCTCGGAGCTGGTGCAGGCTGTGTCCGGATCCCAG
 CTCTCTCTCAATACGGAAAATACCTGACCCTAGAGAATGTGGCTGATCTGGTGAGGGCCATCCC
 CACTGACCCTCCACACGGGTGCAAAAATGGCTCTTGGCAGCCGGAGCCCAAGAAGTGCCTATTCT
 GTGATCACACAGGACTTTCTGACTTGCTGGCTGAGCATCCGACAAGCAGAGCTGCTGCTCCC
 TGGGGCTGAGTTTCATCACTATGTGGGAGGACCTACGGAACCCATGTTGTAAGGTCCCCAC
 ATCCCTACCAGCTTCCACAGGCCTTGGCCCCCATGTGGACTTTGTGGGGGGACTGCACCGT
 TTTCCCCCAACATCATCCTCTGAGGCAACGTCCTGAGCCGCAAGGTGACAGGGACTGTAGGCCCT
 GCATCTGGGGGTAACCCCCCTGTGTGATCCGTAAGCGATACAACCTTGACCTCAACAGACGTGG
 GCTCTGGCACCAGCAATAACAGCCAAGCCTGTGCCAGTTCCTGGAGCAGTATTTCCATGAC
 TCAGACCTGGCTCAGTTCATGCGCCTCTTCGGTGGCAACTTTGCACATCAGGCATCAGTAGC
 CCGTGTGGTTGGACAACAGGGCCGGGGCCGGGCCGGGATTGAGGCCAGTCTAGATGTGCAGT
 ACCTGATGAGTGCTGGTGCCAAATCTCCACCTGGGTCTACAGTAGCCCTGGCCGGCATGAG
 GGACAGGAGCCCTTCCTGCACTGGCTCATGCTGCTCAGTAATGAGTCAGCCCTGCCACATGT
 GCATACCTGTGAGCTATGGAGATGATGAGGACTCCCTCAGCAGCGCCTACATCCAGCGGGTCA
 ACCTGAGCTCATGAAGGCTGCCGCTCGGGGTCTCACCCCTGCTCTTCGCGCTCAGGTGACAGT
 GGGGCCCGGTGTTGGTCTGTCTCTGGAAGACACCAAGTTCCGCCCTACCTTCCCTGCCTCCAG
 CCCCTATGTCACCACAGTGGGAGGCACATCCTTCCAGGAACCTTTCTCATCACAAATGAAA
 TTGTTGACTATATCAGTGGTGGTGGCTTCAGCAATGTGTTCCACAGCCCTTCATACCAGGAG
 GAAGCTGTAAACGAAGTTCCCTGAGCTCTAGCCCCACCTGCCACCATTCCAGTTACTTCAATGC
 CAGTGGCCGTGCTACCCAGATGTGGCTGCACTTTCTGATGGCTACTGGTGTTGGTGAGTGCAGCA
 GAGTGCCCATTCATGGGTGTCCGGAACCTCGGCCCTCACTGACCTGTTTGGGGGGATCCTA
 TCCTTGATCAATGAGCACAGGATCCTTAGTGGCCGCCCCCCCTTTGGCTTTCTCAACCCAAG
 GCTCTACCAGCAGCATGGGGCAGGTCTCTTTGATGTAACCGTGGCTGCCATGAGTCTCTGT
 TGGATGAAGAGGTAGAGGGCCAGGGTTTCTGCTCTGGTCTGGCTGGGATCCTGTAAACAGGC
 TGGGGAACACCAACTTCCAGCTTTGCTGGAGACTCTACTCAACCCTGACCCCTTCTCTATC
 AGGAGAGATGGCTTGTCCCCCTGCCCTGAAGCTGGCAGTTTCACTCCCTTATTCTGCCCTGTG
 GAAGCCCTGCTGAACCCCTCAACTATTGACTGCTGCAGACAGCTTATCTCCCTAACCCCTGAAA
 TCTGTGAGCTTGACTTGACTCCCAACCTACCATGCTCCACTACACTCAGGTCTCCCTACT
 CTGCCTTAGATTCTCAATAAGATGCTGTAACTAGCATTTTTTGAATGCCTCTCCCTCCCG
 ATCTCATCTTTCTCTTTTCAATCAGGCTTTTCCAAAGGGTTGTATACAGACTCTGTGCACTA
 TTTCACTTGATATTCAATCCCAATTCAGTGCAAGGAGACCTCTACTGTACCGTTTACTCT
 TTCCCTACCTGACATCCAGAAACAATGGCCTCCAGTGCATAGTCAATCTTTGCTTTATG
 GCCTTTCCATCATAGTTGCCCCACTCCCTCTCCTTACTTAGCTTCCAGGTCTTAACCTTCTGT
 ACTACTCTTGTCTTCTCTCTCATCAATTTCTGCTTCTTCATGGAATGCTGACCTTCTATTG
 TCCATTGTAGATTTTGTCTTCTCAGTTTACTCATGTGCCCTGGAAACAAATCACTGACA
 TCTACAACCATTCATCTCACTAAATAAGACTTTCTATCCAAATATGATTGATACCTCAAA
 TGTAACAAAA

10904838.071301

FIGURE 94

MGLQACLLGLFALILSGKCSYSPEPDQRRTLPPGWVSLGRADPEEELSITFALRQQNVERLS
ELVQAVSDPSSPQYGKYLTLNVADLVRPSPLTLHTVQKWLALAGAQQKCHSVITQDFLTCWL
SIRQAELLPLGAEFHHYVGGPTETHVVRSPHPYQLPQALAPHVDFVGGGLHRFPPTSSLRQRP
EPQVTGTVGLHLGVTPSVIRKRYNLTSQDVSGGTSNNSQACAQFLEQYFHDSDLAQFMRLFG
GNFAHQASVARVVGQQGRGRAGIEASLDVQYLMSAGANISTWVYSSPGRHEGQEPFLQWLML
LSNESALPHVHTVSYGDDSDLSAYIQRVNTELMKAAARGLTLLFASGDSGAGCWSVSGRH
QFRPTFPASSPYVTTVGGTSFQEPFLITNEIVDYISGGGFSNVFPRPSYQEEAVTKFLSSSP
HLPPSSYFNASGRAYPDVAALSDGYWVVSNRVPIPVVSGTSASTPVFGILSLINEHRILSG
RPPLGFLNPRLYQQHGAGLFDVTRGCHESCLDEEVEGQGFCSGPGWDPVTGWGTPTSQLC

Signal sequence:

amino acids 1-16

N-glycosylation site.

amino acids 210-214, 222-226, 286-290, 313-317, 443-447

Glycosaminoglycan attachment site.

amino acids 361-365, 408-412, 538-542

Casein kinase II phosphorylation site.

amino acids 212-216, 324-328, 392-396, 420-424, 525-529

N-myristoylation site.

amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225,
248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488,
521-527, 533-539, 549-555

[illegible]

MAGIPGLLFLFFLLCAVGQVSPYSAPWKPTWPAAYRLPVVLQOSTNLAKPDFGAEAKLEVS
SSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYLLSSSGDGAQHRDGGSSGKS
RRKRQIYGDSRFSIFGKDFLLNYPFSTSVKLSGTCTGLVAEKHVLTAACHIDHGKTYVKG
TQKLRVGLFKPKFKDGGRGANDSTSAMPEQMFKQWIRVKRTHVPKGWIKGNANDIGMDYDYA
LLELKKPKHRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDETYDLLYQQCD
AQPAGSGSGVYVRMWRKQQQKWERKIIGIFSGHQWDMNGSPDQFNVAVRITPLKYAICIWY
TKGNYLDCDRE

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 93-97, 207-211

Glycosaminoglycan attachment site.

amino acids 109-113, 316-320

Casein kinase II phosphorylation site.

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

N-myristoylation site.

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

Serine proteases, trypsin family, histidine active site.

amino acids 171-177

FIGURE 97

GCATCGCCCTGGGTCTCTCGAGCCTGCTGCCTGCTCCCCGCCCCACCAGCC**ATG**TGGTTT
CTGGAGCGCCCCAGCCCTGGGTGGGGGCTGTCTCGGCACCTTCACCTCCCTGCTGCTGCTG
GCGTCGACAGCCATCCTCAATGCGGCCAGGATACCTGTTCCCCCAGCCTGTGGGAAGCCCCA
GCAGCTGAACCGGGTTGTGGGCGGCGAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGA
GCATCCAGAAGAATGGGACCCACCACTGCGCAGGTTCTCTGCTCACCAGCCGCTGGGTGATC
ACTGCTGCCCATGTGTTTCAAGGACAACCTGAACAAACCATACCTGTTCTCTGTGCTGCTGGG
GGCCTGGCAGCTGGGGAACCTGGCTCTCGGTCCAGAAAGGTGGGTGTTGCCTGGGTGGAGC
CCCACCTGTGTATTCTTGGAAGGAAGGTGCCTGTGACAGACATTGCCCTGGTGCCTCTCGAG
CGCTCCATAACAGTTCTCAGAGCGGTCCTGCCCATCTGCCCTACCTGATGCCCTATCCACCT
CCCTCCAAACACCCACTGCTGGATCTCAGGCTGGGGGAGCATCCAAGATGGAGTTCCTTGC
CCCACCTCAGACCTGCGAGAAGCTGAAGGTTCTATCATCGACTCGGAAGTCTGCAGCCAT
CTGTACTGGCGGGGAGCAGGACAGGGACCCATCACTGAGGACATGCTGTGTGCCGGCTACTT
GGAGGGGAGCGGGATGCTTGTCTGGGCGACTCCGGGGCCCCCTCATGTGCCAGGTGGACG
GCGCCTGGCTGTGCGCCGGCATCATCAGCTGGGGCGAGGGCTGTGCCGAGCGCAACAGGCC
GGGGTCTACATCAGCCTCTCTGCGCACCGCTCCTGGGTGGAGAAGATCGTGCAAGGGGTGCA
GCTCCGCGGGCGCGCTCAGGGGGGTGGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGGCCG
CCGCGCGCTCC**TAG**GGCGCAGCGGGACGCGGGGCTCGGATCTGAAAGGCGGCCAGATCCACA
TCTGGATCTGGATCTGCGGCGGCCTCGGGCGGTTTCCCCCGCGTAAATAGGCTCATCTACC
TCTACCTCTGGGGGCCCCGACGGCTGCTGCGGAAAGGAAACCCCTCCCCGACCCGCCGAC
GGCCTCAGGCCCCCTCCAAGGCATCAGGCCCCGCCAACGGCCTCATGTCCCCGCCCCAC
GACTTCCGCCCCGCCCGGGCCCCAGCGCTTTGTGTATATAAATGTTAATGATTTTTAT
AGGTATTTGTAACCTGCCACATATCTTATTTATCTCCAATTTCAATAAATATTATTAT
CTCCAAAAA

FIGURE 98

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA43318
><subunit 1 of 1, 317 aa, 1 stop
><MW: 33732, pI: 7.90, NX(S/T): 1
MVVSGAPPALGGGCLGTFTSLLLLASTAILNAA RIPVPACGKPKQQLNRVVGGEDSTDSEWP
WIVSIQKNGTHHCAGSLTSTRVITA AHCFKDNLNKPYLFSVLLGAWQLGNPGRSRSQKVGVA
WVEPHFVYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPNTHCWISGWGSIQDG
VPLPHPQTLQKLKVPIIDSEVCSHLYWRGAGQGPITEDMLCAGYLEGERDACLGDSGGPLMC
QVDGAWLLAGIISWGECAERNRPGVYISLSAHRSWVEKIVQGVQLRGRAQGGGALRAPSQG
SGAAARS
```

Signal sequence:

amino acids 1-32

N-glycosylation site.

amino acids 62-66, 96-100, 214-218, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

	(10)		(11)
	(12)		(13)
	(14)		(15)
	(16)		

GACGCGCTGGCCACCATGCACGGCTCCTGCAGTTTCTGTATGCTTCTGCTGCCGCTACTGCTA
 CTGCTGGTGGCCACCACAGGCCCCGTTGGAGCCCTCACAGATGAGGAGAAACGTTTGATGGT
 GGAGCTGCACAACCTCTACCGGGCCAGGTATCCCCGACGGCCTCAGACATGCTGCACATGA
 GATGGGACGAGGAGCTGGCCGCCTTCGCCAAGGCCTACGCACGGCAGTGCCTGTGGGGCCAC
 AACAAAGGAGCGCGGGCGCGCGGCAGAGAATCTGTTTCGCATCACAGACGAGGGCATGGACGT
 GCCGCTGGCCATGGAGGAGTGGCACACGAGCGTGAGCACTACAACCTCAGCGCCGCCACCT
 GCAGCCCAGGCCAGATGTGCGGCCACTACACGCAGGTGGTATGGGCCAAGACAGAGAGGATC
 GGCTGTGGTTCCCACTTCTGTGAGAAAGCTCCAGGGTGTGAGGAGACCAACATCGAATTACT
 GGTGTGCAACTATGAGCCTCCGGGGAACGTGAAGGGGAAACGGCCCTACCAGGAGGGGACTC
 CGTGCTCCCAATGTCCCTCTGGCTACCACTGCAAGAACTCCCTCTGTGAACCCATCGGAAGC
 CCGGAAGATGCTCAGGATTTCGCTTACCTGGTAACTGAGGCCCATCCTTCCGGGCGACTGA
 AGCATCAGACTCTAGGAAAATGGGTACTCCTTCTTCCCTAGCAACGGGGATCTCCGGCTTTCT
 TGGTAACAGAGGCTCTCAGGCTCCCTGGCAACCAAGGCTCTGCCTGTGTGGAAACCCAGGCC
 CCAACTTCTCTTAGCAACGAAGAAGCCGCTCCTTAGCAACAGAGGCTCCCACTTTCGCTAAC
 AACTGAGGTCCCTTCATTTTGGCAGCTCACAGCCTGCCTCCTTGGATGAGGAGCCAGTTA
 CCTTCCCCAAATCGAACCCATGTTCTATCCAAAATCAGCAGACAAGTGACAGACAAAAACA
 AAAGTGCCCTCTAGGAGCCCAGAGAACTCTCTGGACCCCAAGATGTCCCTGACAGGGGCAAG
 GGAATCCTACCCCATGCCCAGGAGGAGGCTGAGGCTGAGGCTGAGTTGCCTCCTTCAGTG
 AGGTCTTGGCCTCAGTTTTTCCAGCCCAAGCAAGCCAGGTGAGCTGCAGGCCACACTGGAC
 CACACGGGGCACCTCCTCAAAGTCCCTGCCAATTTCCCAATACCTCTGCCACCGCTAA
 TGCCACGGGTGGGCGTGCCCTGGCTCTGCAGTCGTCTTGCCAGGTGCAGAGGGCCCTGACA
 AGCCTAGCGTTGTGTACGGGCTGAACCTCGGGCCCTGGTCATGTGTGGGGCCCTCTCTGGGA
 CTACTGCTCCTGCCTCCTCTGGTGTGGCTGGAATCTTCTTGAATGGGATAGCACTCAAAGGG
 TGAAGAGGTACAGTGTCTCTGTCTATCTTCCCCACCTGTCCCCAGCCCCCTAAACAAGATA
 CTTCTTGGTTAAGGCCCTCCGGAAGGGAAAGGCTACGGGCGATGTGCCTCATCACACCATCC
 ATCCTGGAGGACAAAGCCCTGGCTGGCTGCGAGCTCAGGAGGCCGCTGAGGACTGACACAC
 GGGCCACACCTCTCTGCCCCCTCCCTCCTGAGTCCTGGGGGTGGGAGGATTGAGGGAGCT
 CACTGCCTACCTGGCTGGGGCTGTCTGCCACACAGCATGTGCGCTCTCCCTGAGTGCGCTG
 TGTAGTCTGGGGTAGGGATTCCTAGGGGCAGATGAAGGACAAGCCCCACTGGAGTGGGGTTC
 TTTAGTGGGGGAGGACGAGGGAAGGAAAGTAACCTCTGACTCTCCAATAAAAACTT
 GTCCAACCTGTGAAA

FIGURE 100

MHGSCSFLMLLLPLLLLLVATTGPGVGTALDEEKRLMVELHNLRYAQVSPITASDMLHMRWDEE
LAFAKAYARQCVWGHNKRGRGRGENLFAITDEGMDVPLAMEEWHHEREHYNLAAATCSPGQ
MCGHYTQVWAKTERIGCGSHFCEKLQGVETNIELLVCNYEPPGNVKGKRPYQEGTPCSQC
PSGYHCKNSLCEPIGSPEDAQDLPLYLVTEAPSFRAEASDSRKMGTPSSLATGIPAFVLVTEV
SGSLATKALPAVETQAPTSLATKDPSPSMATEAPPCVTTTEVPSILAAHSLPSLDEEPPVTFPKS
THVPIPKSADKVTDKTKVPSRSPENSLDPKMSLTGARELLPHAQEEAEAEELPPSSEVLAS
VFPAQDKPGELQATLDHTGHTSSKSLPNFPNTSATANATGGRALALQSSSLPGAEGDPKPSVV
SGLNSGPGHVWGPLLGLLLPLVLVLAGIF

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 114-118, 403-407, 409-413

Glycosaminoglycan attachment site.

amino acids 439-443

Casein kinase II phosphorylation site.

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

N-myristoylation site.

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237,
250-256

Amidation site.

amino acids 82-86, 172-176

Peroxidases proximal heme-ligand signature.

amino acids 287-298

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.

amino acids 127-138

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.

amino acids 160-172

FIGURE 101

GTAACCTGAAGTCAGGCTTTTCATTTGGGAAGCCCCCTCAACAGAAATTCGGTCATTCTCCAAGTTATGTTGGACGT
 ACTTCTGTGTGTTCTCCCTCTGCTTGCCTTTTCACATATAGCAGACCGGACTTAAGTCACACAGATTATCTTTTCAT
 CAAGGCAAGTTCATGAGCCACTTCAAAGCCTTCGAGAAGTGAACCTGAACCAACATGAATGGAGACATTCC
 AAATCTGGGACAGCTCTCGGCAAAATATTACACTTCTCTCCTTGGCTGGGAAACAGGATTTGTTGAAATACCTCCCTGA
 ACATCTGAAGAGTTTTCAGTCCCTTGAAGACTTTGGACCTTAGCAGCAACAAATATTTAGAGCTCCAAATCGCAT
 TCCAGCCCTACAGCTCAAAATATCTGATATCTCAACAGCAACCGAGTCACATCAATGGAACTCGGGTATTTTGACAA
 TTTGGCCCAACACACTCCTTGTGTGTTAAAGCTTGAACAGGAACCGAATCTCAGCTATCCCAACCAAGATGTTTAAACT
 GCCCAACTGCAACATCTCGAATTTGAACCGAAACAGAGTAAAAATGTAGATGGACATGACATTTCAAGGCCCTTTGG
 TGCTCTGAAGTCTCTGAAATCTCAAAGAAATGGAGTAAACGAACTTTATGGATGGAGCTTTTGGGGGCTGAGCAA
 CATGCAAAATTTTGCAGCTGGACCAATAACAACTTAAACAGAGATACCAAAGGCTGGCTTTACGGCTTCTGATGCT
 GCAGCAACTCTCATCTCAGCCCAAAATGCCATCAACAGGATCAGCCCTGAGTGCCTGGGAGTTCTGCGCAAGCTCAG
 TGAGCTGGACCTTAACCTTTCATCACTTATCAAGGTTAGATGATTCAAGCTTCTTGGCCTTAAGCTTACTAAATAC
 ACTGCACATTTGGGAACACAGAGTCAGCTACATTTGCTGATTTGCGCTTCCGGGGCTTTCCAGTTTAAAGACTTT
 GGATCTGAAGAACATGAAATTTTCCTGGACTATTGAAGACATGAATGGTCTTCTCTGGGCTTGACAAACTGAG
 GCGACTGATATCTCCAGGAAATCGGATCCGTTCTATTACTAAAAAGCCTTCACTGGTTTGGATGCATTTGGAGCA
 TCTAGACCTGAGTGACAAACGAATCATGTCTTTTACAAGGCAATGCATTTTCAAAATGAAGAACTGCAACAACT
 GCATTTAAATACATCAAGCTTTTGGTGGATTTGCCAGCTTAAATGGCTCCCAAGTGGGTGGCGGAAACCACTT
 TCAGAGCTTTGTAATCCGAGTTGTGCCCATCTCAGCTGTCTAAAGGAAGAAGCAATTTTGTCTGTATAGCCAGA
 TGGCTTTGTTGTGTGATGCTTTCCCAACCCAGATCACGGTTCAAGCCCAAGTGGCGGCAATGAGGATTTTCACT
 CAATTTGAGTTTCACTCTGCTCAGCTGGCCAGCAGCTGATTTCCCAATGACTTTTGGTGGAAAAAGACAAATGA
 ACTACTGATGATGCTGAAATGAAAAATTTGCAACCTCCGGCCCAAGTGGCGGCAATGAGGATTTTCACTTACCA
 CATCTTCCGCTGGCGCAGGTGGAATTTGCCAGTGGAGGGAATAATCAGTGTGTCTCTCAATCACTTTGGTTTC
 ATCTCTACTCTGTCAAGAGCAAGCTTACAGTAAATATGCTTCCCTCACTTCAACCAAGCCCAAGTGTGATTTTATCGT
 CCGAGCTGGGGCCATGGCAGCTTGGAGTGTGCTGCTGTGGGGCCACCCAGCCCCAGATAGCTGGCAGAGA
 TGGGGGCACAGACTTCCCACTGCACGGGAGAGACGCATGTCATGTGATGCCAGGATGACGTGTTTCTTATCGT
 GGATGTGAGATGAGGACATTTGGGTATACAGCTGCACAGCTCAGAACAGTGCAGGAAGTATTTTTCAGCAATGC
 AACTCTGACTGTCTGAAGACACCATCATTTTGGCGGCCACTGTTGGAGCCGACTGTAAACCAAGGGAGAAACAGC
 CGTCTCAGCTGCATTTGCTGGAGGAAGCCCTCCCTTAAACTGAACCTGGAACCAAGATGATAGCCCATTTGTTGGT
 AACCAGAGGCACTTTTTCGACAGGCAATCAGCTTCTGATATTGTGGACTCAGATGTGAGTGTGATGCTGGGAA
 ATACACATGTGAGATGCTTAAACCCCTTGGCACTGAGAGAGGAAACGTGCGCTCAGTGTGATGCCACTCCAAC
 CTGCGACTCCCCTCAGATGACAGCCCATCGTTAGACGATGACGGATGGGCGCACTGTGGGTGTCTGATCATAGC
 CGTGGTTTGCCTGTGTGGTGGGCAGCTCACTCGTGTGGTGGTTCATCATATACCACACAAGCGGAGGAATGAAGA
 TTGACGACTTACCAACACAGATGAGACCAACTTGCAGCAGATATCCCTAGTTTGTGTCATCTCAGGGAACGTT
 AGCTCAGGCGAGATGGGTACGTGTCTTCAAGAAATGGAAGCCACCAAGCTTTGTACATCTTCAGGTTCTGG
 ATTTTCTTACCAACATGACAGTGTGGGACCTGCCATATGCAATAGCAATGAGTGAAGCTGATGTGGAGCTGC
 CACAGATGCTTCTTCTTGTAGATTTTGGGATCCAGAGCCCTATGTATTGAAAGGAAATGTGTATGGCTCAGA
 TCCTTTTGAACATATCATACAGGTTGCGAGTCTGACCCAAAGAACAGTTTAAATGGACCACTATGAGCCAGTTA
 CATAAAGAAAAAGGATGCTACCCATGTTCTCATCTTCAAGAATCTCTGCAAGAGGAGCTTCAATATATATC
 GTGGCCTTCACTGTGAGGAGCTACTTAACTAGTTACTCTCAATGAAGGACCTTGAATGAAAAATCTGTG
 TCTAAACAGACTCTCTTGTAGATTTTGTAGTAAATCCAGAGCCAGCGTCTCGGTCTCGATTAATCTTTCATGGG
 TACCTTTTGAAGAACTCTCAGGAGACCTCACCAGATGCTTATCAAGCTTTGGACAGCCATCAGATTGTGAGCC
 AAGAGCTTTTATTTGAAAGCTCACTTCTCCAGACTTGGACTTGGAGTGCAGAGGAAGATGGGAAAGAAAGGAC
 AGATTTTTCAGGAAGAAATACATTTGTACCTTTAAACAGACTTGAAGAACTCAGGACTCCCAATTTTCAGTCT
 TTATGACTTGGACACATAGACTGAATGAGACCAAGGAAAGCTTAACTACTACTCTCAAGTGAACCTTTATTTA
 AAAGAGAGAGATCTATATGTTTTTAAATGGAGTTATGAAATTTAAAGGATGAAATGCTTTATTTATACAGAT
 GAACCAAAATACAAAAGTTATGAAAAATTTTATACCTGGGAATGATGCTATATGAAGATACCTTTTAACTA
 TTTTTTAACCTTGTATTTCTGCAAAAGATATCTTACGTAAATTAATGATATAAATCATGATATTTTATGTATT
 TTATAATGGAGTTTATTTTATGAAAAATGAGTTACTAAAGCATTTTAAATAATCACTGCTTGTACCATTTT
 TTAATAGAGTTACTTCAATATATTTTGCACATTAATTTAATAAAATGTGTCAATTTGAA

00004636.071304

FIGURE 102

MVDVLLLFSLCLLFHISRPDLSHNRLSFIKASSMSHLSQSLREVKLNNNELETIPNLGPVSAN
ITLLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAPFALQLKYLILNSNRVTSMEP
GYFDNLANTLLVLKLNRRNRI SAIPPKMFKLPLQLHLELNRRNKKNVVDGLTFQGLGALKSLKM
QRNGVTKLMDGAFWGLSNMEILQLDHNMLTEITKGWLYGLMLQLHLSQNAINRISPDWE
FCQKLSLELDLTFNHLRLDDSSFLGLSLNLTLLHIGNNRVSYIADCAFRGLSSSLKTLDLKNE
ISWTI EDMNGAFSGLDKLRRLILQGNRIRSI TKKFTGLDALEHLDSLDAIMSLQGNAFSQ
MKKLQQLHLNLTSSSLCDQQLKWL PQWVAENNFQSFVNASCAPHQLLKGRSIFAVSPDGFVCD
DFPKPQITVQPETQSAIKGSNL SFICSAASSDSEPMTPAWKKDNELLHDAEMENYAHRAQG
GEVMEYTTILRLREVEFASEGKYQCVISNHFSSSYSVKAKLTVNMLPSFTKTPMDLTIRAGA
MARLECAAVGHPAPQIAWQKDGDTDFPAARERRMHVMPEDDVFFIVDKIEDIGVYSCTAQN
SAGSISANATLTVLETPSFLRPLLDRTVTTKGETAVLQCIAGGSPPPKLNWTKDDSPLVVTER
HFFAAGNQLLIIVSDSDVSDAGKYTCESNTLGTGRGNVRLSVIPTPTCDSPQMTAPSLDDDG
WATVGVVIIAIVCCVVGTSVLVVVVIYHTRRRNEDCSITNTDETNPADI PSYLSSQGTAD
RQDGYVSSSESGSHHQFVTSSGAGFFLPQHDSSGTCCHIDNSSADVEATDLFLCPFLGSTGP
MYLKGNVYGSDFPFTYHTGCS PDPRTVLMDHYEPSYIKKKBCYPCSHPSSESCERSFSNISW
PSHVRKLNTSYSHNEGPGMKNLCLNKSSLD FSANPEPASVASSNSFMGTFGKALRRPHLDA
YSSFGQPSDCQPRAFYLYKAHSSPDLDGSGSEEDGKERTDFQEENHICTFKQTLNRYRTPNFQS
YDLDT

Signal sequence:

amino acids 1-19

Transmembrane domain:

amino acids 746-765

N-glycosylation site.

amino acids 62-66, 96-100, 214-220, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

system	card	max. speed	max. dist.	max. acc.	max. dec.	max. time
1	10	100	100	100	100	100
2	20	200	200	200	200	200
3	30	300	300	300	300	300
4	40	400	400	400	400	400
5	50	500	500	500	500	500
6	60	600	600	600	600	600
7	70	700	700	700	700	700
8	80	800	800	800	800	800
9	90	900	900	900	900	900
10	100	1000	1000	1000	1000	1000

GGGGAGGAGGAATTCGACCATTAAGAGAGACTTTTCTTTTGTGGTGGTGGCTGTGGGTGCGCTTTGCAAAATG
 AAGGTGACGAGACGACGCTTTCTCTCGAAGACCGCAATCGATGTAATCGATTGTCGACAGAGAGAGAAAGAAC
 GAAGCTCTTTTCTGTAGCCCTGGATCTTAAACAATGTGTATGTGTGCACAGGAGGAGCTTCAAGATGAA
 TAAACAGAGTAGACCCGCGGGGGTGGTGTCTGCATCAATAATAATCTTAAAGCAGCTTGTCCCCCT
 CCACCCGCAAAAAGAGATGATTGAAAGTAAGAACCGAGATCTCAAAGAAAAAAGTATGTTCATTTTCTC
 TATAAGAGAGAAAGCTGAGCCAGGAGATATTTTTGAATTAAGAATTTGGGGCTTTTAAAGAAATAAGAACT
 GGTGTGGTGGTGTCTCTTTCTTTGAAATTTCCACAAGAGGAGAGAAATTAATAATCATCTGCAAGAAGA
 TTTCCAGAGGAGAAAGCTGAATCGCGGACAGTTGAGGCACTGATTGGGGGAGAGAAACACGACGAGCACTGTG
 TTTGTGCGCTATGTACTAAATGACGAGTAATGTGAGTTGGATTTTCTCATCAACCTGCTTTTAAAT
 TTTATATCTTTTGGTATCAAGATCATGCTGCTTTCTCTGTTCTTAAACAGCTGGATTTCCATCTGGATGTGTCT
 GTGATCAGCTTGAATAACAACGTTTGAAATCAGAGAAGACCAACACAGATAAATATGATGATTTGAACAGAT
 GACTCTATATCCACAGCAGATAGATGATGCTAGTTTAAACGGGCCCTATTTGACCCCTGCTTGTGGTGTCT
 GCTGGCTCTTCAACTTCTTGTGGTGGCTGGTCTGGTGGCGCTCAGACCTGCCCTCTGTGTGGCTCTGCAAGCA
 CCAAGTTCAAGCAAGTGAATTTGTTGCGAAAAACCTGCTGGTAGGCTTCGGATGATCTCCACCAACACAGCGCT
 GTGAACCTCATGAGAAACCAATCGAGATCATCAAGGTAGACAGCTTCAAGCACTTGGAGCACTTGGAAATCT
 ACAGTTGTGATGAGGAACCATATCAGAACCAATTGAATTTGGGGCTTCAATGGTTCGTGGCAACCTCAACACTCTGA
 AACTCTTGACATCTGCTCTTACTACACTCCGAATGAGCTTTGTATCTGTCTAAACTGAAGAGCTCTGTGTT
 GGAAGAACCCCACTGAAGAGCACTCCCTCTTATCTCTTAAAGAAATCTCTTCTTGTGGCGCATAGACTTAGG
 GGAATTTGAAGAACTTTTATACATCTCAGAAGGTGCTTTGAAGGTCTGCTCAACTTGGAGTATTGAACTTGCT
 ATGTGCAACTCGGGAATCCCTAACCTACACCGCTCATAAATCATAGTAGAGCTGGATCTTCTGGGATCA
 TTTATCTGCACTCAGCGCTGGCTCTTTCCAGGGTTGTGATCGACTTCAAAATCTGATGATGATACCGCCAGAT
 TCAAGTGTGAACAGGAATGCCCTTTGCAACCTTCACTCATAGTGGAGATCAACCTGGCAACAATAATCTAAC
 ATTACTGCTCATGACCTCTCACTCTCTGTGATCATCTAGAGCGGATATCTTATACATCAAACTCTGGAATCT
 TAACCTGTGACATCATCTGTGCTCAGCTGGTGGATATAAGAACCTGCCCTCGAACACAGCTTGTGTGCGCGGT
 TAAACCTCTCCCAATCAAGGGGGAGGTACATTGGAGAGCTGCAGCAGAAATCTTACTCATGTCATGCTCCGGT
 GATTGTGGAGCCCCCTCGACACTCAATGTCTCAAGGAGCTGGCAGCTTGAGCTGAAATGTGGGGCTCCACATC
 CTTGACATCTGATCTTGTGATTACTCTCAATGAACACGTCATGACATCGGGGCTCAAAAGTCGGGATGCTGT
 GCTCATGATGGTGTAGCTTAAATTTCACAAAATGTAATCTGTGACAGATACAGGCATGTACATGTATGTGTAGTAA
 TCTCGTTGGGAATACTACTGTTCTCAGCCCACTGAAATGTACTGACGACCAACCATCTCTTTCTTCTTATTTT
 AACCTGTCAGTGAAGACTTGAAGACCTCTCAGGATGAGGACCGGACAGATACAATGTGGGTCCCACTCC
 AGTGTGCACTGGGAGACCAACATGTGACCACTCTCTCACACACAGACAGCAAGGTGCAGACAGAAACCTT
 CACCATCCCACTGATGATATAAAGCAGTGGGATCGAGGAATGTAGGAGTCAAGAGATCAACAAATCTCAT
 TGGGTTTGTGGGCACTCACTCATGCTGTCAGTGATGTGCTGATCTTTCTACAGATGAGGAGACGACCA
 TCGGCAAAACACTCAGCGCCCAACAGGACTGTGAAATTTAATGTGGATGTAGATTACGGGAGACACACC
 CTGGAAGGCCCACTGCCATGCTGTCTATCTGAGCTAGGACCACTAACTACTATACTCATCAAAATCTCCCTT
 CAACACACACAACAGTTTACACAAATAATCAATCAACAGTTTCAGGTGATGAACGTTTATGTATCGAATGAA
 CTTCAAAGCAATGTACAAGAGCTCAAACTTAAACATTTACAGTGTACAATAAACCAACAAACAAAAA
 GACACTTTTATAAATGACAAATGACTGGGCTAAATCTCATGTTTCAAAAGAGTGTCTTACAAAAAACA
 AAAAAAGAAAGAAATTTTATTTTATAAATCTATTGTGATCTAAAGCAAAAAA

FIGURE 104

MLNKMTLHPQQIMIGPRFNRALFDPLLVLVLLALQLLVVAGLVRAQTCPSVCSCSNQFSKVIC
VRKNLREVDPDGISTNTRLNLHENQIQI IKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA
NLNTLELFDNRLTTIPNGAFVYLSKLELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLS
YISEGAFEGLSNLYLNLMCNLREIPNLTPLIKLDELDSLGNHLSAIRPGSFQGLMHLQKL
WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLLHNPWNCNDIL
WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAE
LKCRASSTLSVSWITPNGTVMTHGAYKVRIAVLSDGTNLNFTNVTVDQTMGYTCMVNSVGN
TTASATLNVTAATTPFSYFSTVTVETMEPSQDEARTTDNNVGTPPVVDWETTNVTTSLTPQ
STRSTEKTFTIPVTDINSIGIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHRQN
HHAPTRTVEIINVDBEITGDTPMESHLPMPAIEHEHLNHNYSYKSPFNHTTTVNTINSIHSS
VHEPLLIRMNSKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438,
442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
391-397, 422-428, 433-439, 531-537

FIGURE 105

AGCCGACGCTGCTCAAGCTGCAACTCTGTTGCGAGTTGGCAGTTCTTTTCGGTTCCTCTGCTGTTTGGGGGCA
TGAAGGGCTTCGCCCGCGGGAGTAAAGAAAGAAATTGACCGGGCAGCGCGAGGAGGAGCGCCCAACCGCACCCG
GAGGGCGGGCTGCACCTCTCGGCTTGGAAGTTTGTGCGGGGCCCGGAGCGCGCGCGCTGGGAGCTTCGGGTAGA
GACTAGAGCGCTGAGACCGCGATGAGCGCGCGAGCCTCCGTGCGCGCGCGCGCGGGCTGGGGCTGCTGCTGTGC
GCGGTGCTGGGGCGCGCTGGCGCGTCCGACGCGCGGTCCGCGGGGAACTCGCGGAGCTCTCTGGGGAGCGCGG
GAGCGCCCATCGCCCACTACCTGCGCGCTCTCGGGGACCTGCTGGAGTCGAGTCGTAAGCGGCTAGCGCTCTCT
CCCGAGCACTCCCGTCTCGGGTCTGCTGCTGGCTGGAATTAAGTCAACACAGATTATCTTTTCATCAAGGCGAAGTCC
ATGAGCCACCTTCAAAGCCTTCGAGAAAGTGAACCTGAAACAAACAAATGAATTTGGAAGACCAATCCAAATCTGGGACCA
GTCTCGGCACAAATTACCTTTCTCCTTGGCTGGAAACAGGATTTGTAATAATCTCCCTGAACATCTCGTGAACATCA
TTTCAGTCCCTTGAAATCTTTGGACCTTTAGCAGCAACAAATATTTCAGAGCTCCAACTGCATTTCCAGCGCTTACAG
CTCAAAATCTGTATCTCAACAGCAACCGAGTCACTCAATGGAACCTGGGTATTTTGACAATTTGGGCCAACACA
CTCTCTTGTTTAAAGCTGAAACAGGAACCGAATCTCAGCTATCCCAACCCAAAGATGTTTAAACTGCCCAACTGCAA
CATCTCGAATTTGAACCGAAAACAGATTAAAAATGTAGATGGACTGACATTCGAAGCGCTTGCTGCTCTGAAGTCT
CTGAAAATGCAAGAAATGGAAGTAAACGAAATTTATGGATGGAGCTTTTGGGGGCTGAGCAACATGGAAATTTTG
CAGCTGGACCATAAACCACTTAACAGAGATTACCAAGGCTGGCTTTACGGCTTGCTGATGCTGCAGGAACCTTCAT
CTCAGCCAAATGGCATCAACAGGATCAGCGCTGATGCTGGGAGTTCTGCCAGAAGCTCAGTGAGCTGGACCTA
ACTTTCAATCACTTATCAAGGTTAGATGATTCAAGCTTCTTGGCCTAAGCTTACTAATACTGAGCTGAGCTGGG
AACAACAGAGTCACTGATGCTGATTTGTGCTTCCGGGGGCTTCCAGTTTAAAGACTTTGGATCTGAAGAAC
AATGAATTTCTGGACTATTGAAGACATGAATGGTCTTTCTCTGGCCTTGACAACTGAGGCGACTGATATCT
CAAGGAATCGGATCCGTTCTATTACTAAAAAGCCTTCACTGGTTTGGATGCTATGGAGCATCTAGACCTTGAT
GACAACGCAATCATGTCTTTACAGGCAATGACTTTTCAAAATGAAGAACTGCAACAACTTGCAATTTAAATACA
TCAAGCCTTTTGGCGATTTGCCAGCTTAAATGGCTCCCAAGTGGGTGGCGGAAACCACTTTTCAGAGCTTTGTGTA
AATGCGAGTTGTGCCCTCTCAGCTGCTTAAAGGAAGAAGCATTTTGTGCTTTAGCCGAGTGGCTTTGTGTGAT
GATGATTTTCCCAACCCAGATCAGCGTTTCAAGCAGAAACACAGTGGCGCAATAAAGGATTCGAATTTGAGTTTC
ATCTGCTCAGCTGCAGACCGAGCATGTATCCCAATGACTTTTGTGTAAGAAAGACAACTGAGACTGATGAT
GCTGAAGATGGAATTTATGCAACGCTCCGGGCCCAAGGTGGCGAGGTGATGAGATATACCAACCATCTCCGCTGT
CGCGAGGTGGAATTTGCGCAGTGGGGGAAATACAGTGTGTCATCTCCAATCACTTTGGTTTACTCTACTCTGTCT
AAAGCCAAGCTTACAGTAAATGCTTCCCTCATTCACCAAGACCCCAAGATGATTCACCATCCGAGCTGGAGCC
ATGCGAGCTTGGAGTGTGCTGTGCTGGGGCACCGACCCCAAGATGCTGCGAGAGGTGGGGGACAGT
TTCGAGCTGCACGGGAGAGCGATGATGTGATGCCGAGGATGACGTGTTCTTTATCTGGATGTGAAGATA
GAGGACATTTGGGTATACAGCTGCACAGCTCAGAACAGTCAAGGAATTTTACAGCAATGCAACTGACTGATCT
CTAGAAGCAACATCATTTTTCGGGCACTGTGTGACGCAACTGTAAACAAAGGAGAAACAGCGCTCTACAGTGC
ATTGCTGAGGAAGCCCTCCCTCTAACTGAAGCTGACCAAGATGATAGCCCATTTGTGGTAAACGAGAGGAC
TTTTTTGCGACGAGCAATCAGCTTTGATATTATTTGGAGTCAAGTGTGATGCTGATCCCACTCCAACTCGCACTCCCT
ATGCTAAACCCCTTGGCACTGAGAGGAGAAACGTCGCGCTCAGTGTGATCCCACTCCAACTCGCACTCCCT
CAGATGACAGCCCATCTGTTAGACGATGACGAGTGGGCCATCTGGGGTCTGGATCATATAGCCGCTGGTCTGT
GTGGTGGGACGCTCACTCGTGTGGTGGTCAATCATATACCAACAGGCGGAGGAATGAAGATTGACAGCATATCC
AACAACAGATGAGACCACTTCCGACAGATATTCTTAGTTATTGTGTCATCTCAGGAACTGAGCTGACAGGAG
GATGGGTACGTGCTTTCAGAAATGGGAGGCCACCACTGTTGTGTCATCTTCAGGTCGTTGATTTTCTTGAACA
CAACATCAGAGTATGGGAGCTGCCATATTGACAAATAGCAGTGAAGCTGATGGAAGCTGCCACAGATCTGTCT
CTTTGTCCGTTTTCGGGATCCACAGGCCATATGATTTTGAAGGGAATTTGATTTGGCTCAGATCTCTTTTGAACA
TATCATACAGTTTGGAGTCTGACCCCAAGAACAGCTTTAATGGACCACTATGAGCCCAATTCATAGAAGAAAAAG
GAGTGTACCCATGTTCTCATCTCTCAGAAAGATCTGCGAAGCGGACTTCAGTAATATATCTGCGGCTCTCAT
GTGAGGAGAGCTTAAACATGATGTTCTCACAATGAAGGACCTGGAATTAAGATCTGTGTTAAACAAAGTCC
TCTTTAGATTTTAGTGCAATTCAGAGCGCAGCGTGGTGGCTCGAGTAACTCTTTCAGTGGTACCTTTGAAAAA
GCTCTCAGGAGACTCCTCAGATGCTTAAACAGCTTTAAGAACTACAGGACTCCAACTTCAGTCTTATGACTTGGAC
ATGAACTCAGATTTTCCCGAGACTTGGACTCTGGTTCAGAGGAAGATGGGAAAGAAAGGACAGATTTTCAGGAA
GAAATCAGATTTGTATCTTAAACAGCTTTAAGAACTACAGGACTCCAACTTTTCAGTCTTATGACTTGGAC
ACATAGACTGAATGAGACCAAGGAAAGCTTAAACATACCTCAAGTGAATCTTTATTTAAAGAGAGAGAGAT
CTTATGTTTTTAAATGGAGTATGATTTTAAAGGATAAAAATGCTTTTATATACAGTACAGTACCAAAATAC
AAAAAGTTATGAAAAATTTTATACGTGGGAATGATGCTCATATAAGAATACCTTTTAAACTATTTTTAACTTTG
TTTTATGCAAAAGATGATCTTACGTAAATTAATGATATAAATCATGATTTTATTTATTAATGCGGACA
TTTCTTTTATGAAAAATGAGTTACTAAAGCATTTTAAATAATACCTGCTTTGACCATTTTAAATAGAAAGT
ACTTCACTATATTTCGACATTAATAATTAATAAATGCTCAATTTGAAAAAAGAAAAAAGAAAAAAGAAAAA

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FIGURE 106

MSAPSLRARAAGLGLLLCAVLGRAGRSDDSGRGELGQPSGVAAERPCPTTCRCLGDLDDCSR
KRLARLPPEPLPSWVARLDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVSANIT
LLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFFALQLKYLNLNSNRVTSMEPGY
FDNLANTLLVLKLNRRNRISAIPPKMKFLPOLQHLELNRNRIKIVDGLTFQGLGALKSLKMQR
NGVTKLMDGAFWGLSNMEIQLDHNHNLTEITKGWLYGLLMLQELHLSQNAINRISPDAWFC
QKLSLELDTFNHLSRLDDSSFLGLSLLNLTHIGNNRVSYIADCAFRGLSSLKTLDDLKNEIS
WTIEDMNGAFSGLDKLRRLILQGNRIRSITKKAFTGLDALEHLDSLDAIMSLQGNFASQMK
KLQQLHLNTSSLLCDQLKWLFPQWVAENNFQSFVNASCAHPQLLKGRSIFAVSPDGFVCDDE
PKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKNELLHDAEMENYAHLLRAQGG
VMEYTTILRLREVEFASGKYQCVISNHFSSSYSVKAKLTVNMLPSFTKTPMDLTIIRAGAMA
RLECAAVGHAPQIAWQKDGDTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSTAQNSA
GSISANATLTVLETPSFLRPLLDRTVTVKETAFLQCIAGGSPPKLNWTKDDSPLVVTERHF
FAAGNQLLIIVDSVSDAGKYTCMSNTLGTGERGNVRLSVIPTPTCDSPQMTAPSLDDDGWA
TVGVVIAVCCVVGTSVLVWVVIYHTRRRNEDCSIINTDETNPADIPSYLSSQGTLDADR
DGYVSSSESGSHHQFVTTSSGAGFFLPQHDSSGTCHIDNSSADVAATDLFLCPFLGSTGPMY
LKGNYVGSDDPFETYHTGCSFDDPRTVLMDHYEPSYIKKKECYPCSHPSEESCERSFSNISWPS
HVRKLLNTSYSHNEGPGMKNLCLNKSSLDPSANPEPASVASSNSFMGTGFKALRRPHLDAYS
SFGQPSDCQPRAFYLKAHSSPDLDGSGSEEDGKERTDFQENHICTFKQTLNRYTPNFQSYDLDT

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 808-828

N-glycosylation site.

amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519,
688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020

Glycosaminoglycan attachment site.

amino acids 886-890

Casein kinase II phosphorylation site.

amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378,
383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735,
799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022,
1073-1077, 1079-1083, 1081-1085

Tyrosine kinase phosphorylation site.

amino acids 667-675

N-myristoylation site.

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433,
513-519, 588-594, 672-678, 683-687, 774-780, 933-939

Leucine zipper pattern.

amino acids 58-80, 65-87

FIGURE 107

CAAAACCTTGCCTCGCGGAGAGCGCCACGCTTGACTTGAATGGAAGGAGCCCGAGCCCGCGGAGCGCAGCTGAGAC
TGGGGGAGCGCTTGCGCCCTGTGGGGCGCCGCTCGCGCGCGGGGCGCAGCAGGGAAGGGGGAAGCTGTGGTCTGCC
CTGCTTCACGAGGCGCACTGGTGTGAAACGGGAGAGCCCTGGGTGGTCCCGTCCCTATCCCTCCTTTATATA
GAAACCTTCCACACTGGGAAGGCGAGCGCGAGGCGAGGAGGCTCATGGTGAGCAGGAGGCGCGCTGATCTGCAG
GCGCACAGCAITTCGAGTTTACAGATTTTACAGATACCAAATGGAAGGCGAGGAGGCAGAACACAGCTGCCCTGGT
TCATACAGCCCTGGCGCCACAGGCGCATCTGACTCGGCACCCCTGCAAGGCACATGGCCACAGGCGGGTCTGTC
TGCTCTGTGCTGCTGCGCGCAACAGCTGCACCTGGGACCTGTGCTTGGCTGGAGGGCCCGAGGATTTGGCCGAA
GTGGCGGCGCACAGCTGAGCCCGCAAGAGAAACGAATTTGGGAGGAGGAGCGGTGTCTGTACTGAGCCCTGAGG
AGCCCGGGCTGGCCAGCGCGGCTCAGCTGCCCCGAGACTGTGCTGTGTCCAGGAGGGCGTGTGGGACTGTG
GCGGTATGACCTGTGTGAGTTCCCGGGGACCTGCCTGAGCACACCAACCACTATCTCTGCAGAACCAACGAC
TGGAAAGATCTACCTCTGAGGAGCTTCCGGGCTGACCGGCTGGAGACTGAACTGCAAAAACAAACCGCTGA
CTTCCGAGGGCTCCAGAGAAAGCGCTTGTAGCATCTGACCAACCTCAATTACCTGTACTTGGCCAAATAACAGC
TGACCTTGGCACCCGCTTCTCTGCCAAACGCCCTGATCAGTGTGGACTTTGTCTGCCAATATCTCAACGAATCT
ATGGGCTCACCTTTGGCCAGAAGCCAAACTTGAGGTCTGTGTACCTGCACAAACCAAGCTGGCAGACGCGGGC
TGCCGAGCAACATGTTCAACGGCTCCAGCAACGTTCGAGGTCTCATCTGTCTGACCACTTCTCTGCGCCAGCTGC
CCAAGCACTTGCAGCTGCCCTGTACAGCTGCACCTCAAGAACCAACAGCTGGAGAAAGATCCCGCCGGGGCT
TCAGCGAGCTGAGCAGCCTGCGGAGCTATACCTGCAGAACCACTACCTGACTGACGAGGGCTGGACCAACGAGA
CCTTCTGGAAGCTCTTCAGGCTGGAGTACCTGGATCTGTCTGACCAACCACTTGTCTCGGCTCCAGCTGGGCTGC
CGCGCAGCTGGTGTCTGTGCTCTTGGAGAAGAACGCCATCCGAGCGTGGACGCGAATGTGCTGACCCCATCC
GCAGCTGGGTGATCTCTGCTGCTGCACAGCAACAGCTGCGGAGCAGGCGATCCACCCATGGCTCTCCAGGGC
CTAAGCGTTGACACCGGTGACCTTGTACAAACACGCGTGGAGCGCTGCCAGTGGCTCTCTGCGCGCTGC
GCACCCCTATGATCTCTGCACCAACAGATCACAGCATTTGGCCGGAAGACTTGGCCACACACTACTTCTCTGGAGG
AGCTCAACCTCAGTGCACAAACGATCACAGCCACAGCTGCAGTGACCGCGACCGCTTCCGCAAGCTCGCGCTGTGC
GCTCGCTGGAACCTGTGCGGCAACCGGCTGCACACGCTGCCACCTGGGCTGCCCTGAAATGTCCATGTGTGAAG
TCAAGCCCAATGAGCTGCTGCTTGGSCACGAGGGGCGCTGGCGGSCATGGCTCAGCTGCGTGAGCTGTACCTCA
CCAGCAACCGCTGCGCAGCGAGCCCTGGGCGCCCGTGTGCTGGTGGACTCTCGCCATCGCTGCTGCTGGACA
TCGCGCGGAATCAGCTCAGCAGAGATCCCGGAGGGGCTCCCGAGTCACTTGTAGTACCTGTATCTCAGAAACA
AGATTAGTGTGCGTGCCTCGCCAACTTCCGACTTCCACGCCCAACCTCAAGGGCTCTTCTCAGGTTTAAACAAGC
TGGCTGTGGGCTCCGTGGTGGACAGTGCCTTCCGAGGCTGAAGCACCTGACAGTCTTGGACATTGAAGGCACT
TAGAGTTTGGTGACATTTCCAGGACCGTGGCGCTTGGGGAAGGAAAGGAGGAGGAGGAGGAGGAGGAGGAGG
AGGAAGAGGAAACAAGATAGTGACAAAGTGATGCAGATGTGACTTAGGATGATGGACCGCGGACTCTTTCTGTC
AGCACACGCTGTGTGCTGTGAGCCCCCACTCTGCGGTGTCTACACAGACACACCCAGCTGCACACATGAGGCA
TCCACATGACACGGGCTGACACAGTCTCATATCCCAACCCCTTCCACGCGGTGTCCACGCGCAGACACATGC
ACACACATCACACCTCAAACACCCAGCTCAGCCACACACAACTACCTCCAAACACCACTGCTCTGTGCACAC
CCCCACTACCGCTGCACGCGCTCTGAATCATGACGGGAAGGGTCTGCCCTCGCCCTGGCCACACACAGGCAACCA
TTCCTCTGCTGCTGCTTCCCTGGAGAAAGACAAAGGTATCCATACACACCAACACACACACATGCAACAGTCAITGTGCGAA
CAGCCCTCCAAAGCCTATGCCACACAGACAGCTCTTGCACCGCCAGAAATCAGCCATAGCAGCTCGCGCTGTGCTCT
TGCCACCTGTGCTGCTTCCCTGGAGAAAGACAAAGGTATCCATCTGTGCTGAGGCTCCCTCTGACCGCTTCTGCT
GGAACCTCAAAAGCTGGCTTTTATCTCTTCCATCTTATGGGACAGGAGCCTTCAAGCATGTGCGCTTGGCC
TGGCCACCTGCTCTCCAGGTGTGGCGAGTCACTGTCTAAGAGTCCCTCTGCGCACCGCCCTGGCAGGACA
GAGGCACTTTTCAATGGGCAAGCCAGTGGAGGACAGGATGGGAGAGCCCTTGGGTGCTGTCTGGGCGCTTGGGG
CAGGAGTGAAGCAGAGGTGATGGGCTGGCTGAGCAGGGAGGAGGAGCCAGCTGCACCTAGGAGACACCTTT
GTTCTTCAGGCTGTGGGGAGGTTTCGCGGTGCTTTATTTTATTTCTTTTAAAGAAAAAATGATAAAAAAT
CTCAAGCTGATTTTCTTGTATAGAAAACTAATATAAAGCAATTACCTATCCCTGCAAAAAA

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FIGURE 108

MEGEEAEQPAWFHQPWPRGASDSAPPAGTMAQSRVLLLLLLLLPPQLHLGPVLAVRAPGFGRS
GGHSLSP EENEFAEEEEPVLVLSPEEPGPGPAAVSCPRDCACSQEGVVDCGGIDLREFPGDLP
EHTNHLSLQNNQLEKIYPEELSRHLRLETLNLQNNRLTSRGLPEKAFEHLTNLNYLYLANNK
LTLAPRFLPNALISVDFAANYLTKIYGLTFGQKPNLRSVYLHNNKLADAGLPDNMFGSSNV
EVLILSSNFLRHVPKHLPPALYKLHLKNNKLEKIPPGAFSELSSRLRELYLQNNYLTDEGLDN
ETFWKLSSLEYLDLSSNNLSRV PAGLPRSLVLLHLEKNAIRSVDANVLTPIRSLEYLLHLSN
QLREQGIHPLAQGLKRLHTVHLYNNALERVPSGLPERRVRTLMILHNQITGIGREDFATYF
LEELNLSYNRLITSPQVHRDAFRKLRLRLSLDLSGNRLHTLPPGLPRNVHVLKVKRNELAALA
RGALAGMAQLRELYLTSNRLRSRALGPRAWVDLAHLQLLDIAGNQLTEIPEGLPESLEYLYL
QNNKISAVPANAFDSTPNLKGIFLRFNKLAVGSVVDSAFRRLKHLQVLDIEGNLEFGDISK
RGRLGKEKEEEEEEEEEEEETR

Signal sequence:

amino acids 1-48

N-glycosylation site.

amino acids 243-247, 310-314, 328-332, 439-443

Casein kinase II phosphorylation site.

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

N-myristoylation site.

amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,
477-483, 498-502, 539-545, 548-554

Leucine zipper pattern.

amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,
535-557

FIGURE 109

GGGAGGGGGCTCCGGGCGCCGCGCAGCAGACCTGCTCCGGCCGCGCGCTCGCCGCTGTCTCCGGGAGCGGCAG
CAGTAGCCCCGGGCGCGAGGGGCTGGGGGTTCTCTCGAGACTCTCAGAGGGGCGCTCCCATCGCGCCCAACACCC
CAACCTGTTCTCGCGCGCCCACTGCGCTGCGCCCGCCAGGACCCGCTGCCCAA**CTGGAT**TTTTCTCTGGCGCTGGT
TGCTGGTATCTCGCTCTACCTGCAAGCGCGCGCGCGAGGTTGCAAGGGAGGTGCCCGCAGCAAAATAGTGTATCGAT
TGCGCTATGTCTGTTATGGTGGGAGGATTGACTGCTGCTGGGCTGGGCTGCGCAAGTCTTGGGGACAAGTGTACGCC
TGTGTGCCAACCAAGATGCAAAACATGGTGAATGTATCGGGGCCAAACAAGTGTCAAGTGTATCTCGTGTATGTCTGG
AAAAACCTGTAAATCAAGATCTAAATGAGTGTGGCCTGAAGCCCGCCGCTGTAAAGCACAGGTGCATGAACACTTA
CGGCAGCTCAAGTGCTACTGTCTCAACGGATATATGCTCATGCCGGATGGTCTCTGCTCAAGTGCCTTGACCTG
CTCCATGGCAAACTGTCAAGTATGGCTGTGATGTTGTTAAAGGACAAATACGGTGCCAGTGCCCATCCCTGGCCCT
GCACCTGGCTGCTGATGGGAGGACTGTGTAGATGTTGATGAATGTGCTACAGGAAGAGCCCTCTGCTGCTATGAT
TAGGCAATGTGTCAACCTTTTGGGAGCTACATCTGCAAGTGTATAAAGGCTCTGATCTCATGTATATTTGGAGG
CAAAATATCAATGTCAATGACATAGACGAATGCTCACTTGGTCAATGATGACGAGCTTGTCTGATGTTATATA
CGTACGTGGGTCTCAAGTGCAAATGTAAAGAAGGATACAGGGTGTATGGACTGACTTGTGTGTATATCCCAAA
AGTTATGATTGAACCTTCAGGTCCAATTCATGTACCAAGGGGAAATGGTACCATTTTAAAGGGTGACACAGGAAA
TAATAATTGGATTCTCTGATGTTGGAAAGTACTTGGTGGCCTCCGAAGACACCATATATTCTCTCATATTACCAA
CAGGCGCTACTTCTAAGCCAAACAAGACCTACACCAAGGCCAACACCAATTCCTACTCCAACACACACACACC
CCTGCCAACAGAGCTCAGAACACCTCTACCACCTACCAACCCAGAAAGGCCAACACCCGACTGACAACTATAGC
ACCAGCTGCCAGTACACCTCCAGGAGGGATTACAGTTGACAAACAGGGTACAGACAGACCTCAGAAACCCAGAGG
AGATGTGTTCAAGTGTCTGGTACACAGTTGTAATTTTGACCATGGAGCTTGTGGATGGATCAGGGAGAAAGACAA
TGACTTGCACTGGGAACCAATCAGGGAGCCAGCAGGTGGACAAATATCTGACAGTGTGGGAGCAAGGCCCGGAG
GGGAAAAGCTGCACGCTTGGTGTCTACCTCTCGCGCGCTCATGTCATTGAGGATGGATCAGGGAGAAAGACAA
CAAGGTGACCGGGCTGCACCTCTGGCACACTCGAGGTGTTTGTGAAGAAACAGGTGCCACAGGACGACCCCTGTG
GGGAAGAAATTTGGTGGCCATGGCTGGGAGGCAACACAGATCACTTGTGAGGGGCTGACATCAAGAGCGCAATCAG
AAGAT**GTAT**TAAAGGCTTGGAAAAAAGATCTATGATGAAAATTAAGAGAACTGGGATATTAGACCTGGAGAG
AGAGACTGAGGGCGCAACCATTGATGGTGTTCAGATATATGAAGGTTGGCACAAGAGGGTGGCCACAGCTG
TTCTCCATATGCACTAAGAATAGAACCAAGAGGAACTGGCTTAGACTAGATTAAGAGAGCATTTCTTGGCAGG
GGCCATTTGATGAATATCTCATAAAAAAGAGGTGTGAAGAACTCTCAGATATCTCTCTCTTTCTAAAAAATTTAGA
TAAAAATTTGTCTATTATTAAGATGGTTAAAGATGTTCTTACCAGGAAAGATTAACAAATATAGAAATTTCCAAA
AGATGTTTGTCTCTACTAGTAGTATGTCAGTGAATACTTTAGAACTAAATAATTTGGACAAGGCTTAATTTAGG
CATTTCCCTCTTGACCTCTAATGGAGAGGGATTGAAAGGGGAAGAGCCACCAAAATGCTGAGCTCACTGAAATA
TCTCTCCCTTATGGCAATCTCAGATATTAAAGAAAAAAGGAAACTATTATTCCAAATGAGAGTATGATGGAC
AGATATTTTAGTATCTCAGTAATGCTCTAGTGTGGCGGTGGTTTCAATGTTCTCATGGTAAAGGTATAAGCC
TTTCATTGTTCAATGGATGATGTTTCAGATTTTCTTTTAAAGAGATCTCAGGAAACACAGTTTCAGAGAG
ATTTTCATCGGGTGCAATCTCTCTGCTCTGTTGTGTGACAAGTTATCTTGGCTGTGAGAAAGAGTGGCCCTGCCCC
ACACCGGCGAGACCTTCTCTCACTCATCAGTATGATTGATTCTCTTATCAATTTGAGCTCTCCAGGTTCCAC
AGAACAGTAAATATTTTGAACAAATAGGTACAATAGAAGGTCTCTGCTATTTAACCTGGTAAAGCGAGGGCTGG
AGGGGGAATAAATCATTAAGCCTTGTAGTAACGGCAGGAATATATGGCTGTAGATCCATTTTAAATGGTTCATT
TCTTTATGGTCATATACTAGCTGAAGATGAAGAGGGGAAAAATAAATGAAATTTTACTTTTCATGCGCAA
TGATACATTGCACTAACTGTAGGAAGAGTTATCCAAAGTACTGTATAACATCTGTTTATTTATTTAATGTTT
CTAAAAATAAAATTTATGTTGTTTCCAAATGGCCATAAAAAACAATTTTGTAAATAAACAACACTGTTAGTATAT

FIGURE 110

MDFLALVLVSSLYLQAAAEFDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPVCQP
RCKHGEICIGPNKCKCHPGYAGKTCNQDLNECGLKPRPCKHRCMNITYGSYKCYCLNGYMLMPD
GSCSSALTCSMANCQYGCDVVKQIQCPSPGLHLAPDGRTCVDVDECATGRASCPRFRQC
VNTFGSYICKCHKGFIDLMIYIGGKYQCHDIDECSLGQYQCSSFARCYNVGRGSYKCKCKEGYQG
DGLTCVYIPKVMIEPSGPIHVPKGNNGTILKGDGTGNNNWI PDVGSTWWPPKTPYIPPIITNRP
TSKPTTRPTPKPTPIPTPPPPPLPTELRTPLPPTTPERPTTGLTTIAPAASTPPGGITVDN
RVQTDPOKPRGDVFSVLVHSCNFDHGLCGWIREKNDLHWEPIRDPAAGQYLTVSAAKAPGG
KAARLVPLPLGRLMHSGLCLSFHVKVTGLHSGTLQVVRKHGAHGAALWGRNGGHGWRTQI
TLRGADIKSESQR

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 273-277

Casein kinase II phosphorylation site.

amino acids 166-170, 345-349

Tyrosine kinase phosphorylation site.

amino acids 199-206

N-myristoylation site.

amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,
421-427, 433-439, 462-468, 476-482

Aspartic acid and asparagine hydroxylation site.

amino acids 104-116, 186-198, 231-243

Cell attachment sequence.

amino acids 382-385

EGF-like domain cysteine pattern signature.

amino acids 75-87

FIGURE 111

CTTCTTTGAAAAGGATTATCACCTGATCAGGTTCTCTCTGCAATTTGCCCTTTAGATTGTGA
AAATGTGGCTCAAGGCTTTACAACTTTCCCTTTCCCTTTGCAACAGGTGCTTGCTCGGGGCTGA
AGGTGACAGTGCCATCACACACTGTCCATGGCGTCAGAGGTCAGGCCCTCTACCTACCGGTC
CACTATGGCTTCCACACTCCAGCATCAGACATCCAGATCATATGGCTATTGTGAGAGACCCCA
CACAATGCCAAATACTTACTGGGCTCTGTGAATAAGTCTGTGGTTCCTGACTTGGAATACC
AACACAAGTTCCCATGATGCCACCCAAATGCATCTCTGCTTATCAACCCACTGCAAGTTCCCT
GATGAAGGCAATTACATCGTGAAGGTCAACATTCAGGGAAATGGAACCTATCTGCCAGTCA
GAAGATACAAGTCACGGTTGATGATCCTGTCAAAAGCCAGTGGTGCAATTATCCTCTCCCT
CTGGGGCTGTGGAGTATGTGGGGAACATGACCCTGACATGCCATGTGGAAGGGGGCACTCGG
CTAGCTTACCAATGGCTAAAAAATGGGAGACCTGTCCACACCAGCTCCACCTACTCCTTTTC
TCCCAAAACAATAACCTTCATATTTGCTCCAGTAACCAAGGAAGACATTGGGAATTACAGCT
GCCTGGTGAGGAACCTGTGAGTAAATGGAAGTGATATCATTATGCCCATCATATATTAT
GGACCTTATGGACTTCAAGTGAATTTGATAAAGGGCTAAAAAGTAGGGGAAGTGTTTACTGT
TGACCTTGGAGAGGCCATCCTATTTGATTGTTCTGCTGATTCTCATCCCCCAACACCTACT
CCTGGATTAGGAGGACTGACAATACTACATATATCATTAAAGCATGGGCCCTCGCTTAGAAGTT
GCATCTGAGAAGTAGCCCAAGACAATGGACTATGTGTGCTGTGCTTACAACAACATAAC
CGGCAGGCAAGATGAAACTCATTTACAGTTATCATCACTTCCGTAGGACTGGAGAAGCTTG
CACAGAAAGGAAAATCATTGTCACTTTAGCAAGTATAACTGGAATATCACTATTTTGTATT
ATATCCATGTGTCTTCTCTTCTATGGAAAAAATATCAACCCCTACAAAGTTATAAAACAGAA
ACTAGAAGGCAGGCCAGAAACAGAATACAGGAAAGCTCAAAACATTTTCAGGCCATGAAGATG
CTCTGGATGACTTCGGAATATATGAATTTGTTGCTTTTCCAGATGTTTCTGGTGTTTCCAGG
ATTCCAAGCAGGTCTGTTCCAGCCTCTGATTGTGTATCGGGGCAAGATTTGCACAGTACAGT
GTATGAAGTTATTCAGCACATCCCTGCCAGCAGCAAGACCATCCAGAGTGAACCTTTCATGG
GCTAAACAGTACATTCGAGTGAATTTCTGAAGAAACATTTTAAGGAAACAGTGGAAAAAGT
ATATTAATCTGGAATCAGTGAAGAAACAGGACCAACACCTCTTACTCATTATTCTTTTACA
TGCAGAAATAGAGGCATTTATGCAAAATGAACTGCAGGTTTTTTCAGCATATACACAATGTCTT
GTGCAACAGAAAAACATGTTGGGGAATATTCCTCAGTGGAGAGTCGTTTCTCATGCTGACGG
GGAGAACGAAAAGTGACAGGGGTTTCTCATAGTTTGTATGAAATATCTCTACAAACCTCA
ATTAGTTCTACTCTACATTTCACTATCATCAACACTGAGACTATCCTGTCTCACTACAA
TGTGGAAACTTTACATTGTTTCGATTTTTCAGCAGACTTGTTTTATTAATTTTATTAGTG
TTAAGAATGCTAAATTTATGTTTCAATTTTATTTCCAAATTTCTATCTTGTATTGTACAA
CAAAGTAATAAGGATGGTTGTCAAAAAACAAACTATGCCTTCTCTTTTTTTTCAATCACC
AGTAGTATTTTTGAGAAGACTTGTGAACACTTAAGGAAATGACTATTAAAGTCTTATTTTTTA
TTTTTTTCAAGGAAAGATGGATTCAAATAAATTATTCGTGTTTTGCTTTTAAAAA

FIGURE 112

MWLKVFTTFLSFATGACSGLKVTVPSTVHGVGRQALYLPVHYGFHTPASDIQIIWLFERPH
TMPKYL LGSVNKSVVPDLEYQHKFTMMPPNASLLINPLQFPDEGNYIVKVN IQNGT L SASQ
KIQVTVDDPVT KPVVQIHPPSGAVEYVGNMTLTCHVEGGTRLAYQWLKN GRPVHTSSTYSFS
PQNNTLHIAPVT KEDIGNYSCLVRNPVSEMESDIIMPIIYYGPGYGLQVNSDKGLKVG EVFTV
DLGEAILFDCSADSHPPNTYSWIRRTDNTTYIIKHGPRLEVASEKVAQKTM DYVCCAYNNIT
GRQDETHFTV IITSVGLEKLAQKGKSLSP LASITGISLFLIISMCLLFLWK KYQPYKVIKQK
LEGRPETEYRKAQTFSGHEDALDDFGIYEFVAFP DVSGVSRI PSRSPASDCVSGQDLHSTV
YEVIQHIP AQQQDHPE

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 341-359

N-glycosylation site.

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208,
276-280, 308-312

Casein kinase II phosphorylation site.

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

Tyrosine kinase phosphorylation site.

amino acids 272-280

N-myristoylation site.

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237,
239-245

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 113

GCAAGCGGCGAAATGGCGCCCTCCGGGAGTCTTGACAGTTCCCTGGCAGTCTGTGGTGTGT
GCTTTGGGGTCTCCCTGGACGACCGGGCGGCGGAGCAACGTTTGCCTCATCACGGACGAGA
ACTGGAGAGAAGTCTGGAGGAGACTGGATGATAGAATTTATGCCCCGTGGTGCCTGCT
TGTCAAAATCTTCAACCGGAATGGGAAAGTTTGTGTAATGGGGAGAAGATCTTGAGGTTAA
TATTGCGAAAGTAGATGTACAGAGCAGCCAGGACTGAGTGGACGGTTTATCATAACTGCTC
TTCCCTACTATTTATCATTGTAAGATGGTGAATTTAGGCGCTATCAGGGTCCAAGGACTAAG
AAGGACTTCATAAACTTTATAAGTGATAAAGAGTGAAGAGTATTGAGCCCCGTTTCATCATG
GTTTGGTCCAGGTTCTGTTCTGATGAGTAGTATGTCAGCACTCTTTCAGCTATCTATGTGGA
TCAGGACGTGCCATAACTACTTTATTGAAGACCTTGGATTGCCAGTGTGGGATCATATACT
GTTTTTGTCTTTAGCAACTCTGTTTTCCGGACTGTTATTAGGACTCTGTATGATATTTGTGGC
AGATTGCTTTGTCTTCAAAAAGGCGCAGACCACAGCCATACCCATACCTTCAAAAAAT
TATTATCAGAATCTGCACAACCTTTGAAAAAAGTGGAGGAGGAACAAGAGGCGGATGAAGAA
GATGTTTCAGAAGAAGAAGCTGAAAGTAAAGAAGGAACAACAAAGACTTTCCACAGAATGC
CATAAGACAACGCTCTCTGGGTCCATCATTGGCCACAGATAAATCC**TAG**TTAAATTTTATAG
TTATCTTAATATTATGATTTTGATAAAAACAGAAGATTGATCAITTTGTTTGGTTTGAAGTG
AACTGTGACTTTTTTGAATATTGCAGGGTTTCTAGCTAGATTGTCATTAAATTTGAAGAGTCTA
CATTCAGAACATAAAAGCACTAGGTATACAAGTTTGAATATGATTTAAGCACAGTATGATG
GTTTAAATAGTTCTCTAATTTTGA AAAATCGTGCCAAAGCAATAAGATTATTGATATATTTGT
TTAATAATAACCTATTTCAGTCTGAGTTTTGAAAAATTTACATTTGCCAAGTATTGCAATTAT
TGAGGTATTTAAGAAGATTATTTTAGAGAAAAATATTTCTCATTTGATATATAATTTTCTCTG
TTTCACGTGTGAAAAAAGAAGATATTTCCCATAAATGGGAAGTTTGGCCATTGTCTCAAG
AAATGTGTATTTAGTGACAATTTCTGGTCTTTTTAGAGGTATATTCAAAATTTCCCTGT
ATTTTTAGGTTATGCAACTAATAAAACTACCTTACATTAATTAATTACAGTTTTCTACACA
TGGTAATACAGGATATGCTACTGATTAGGAAGTTTTTAAGTTCATGGTATTCTCTTGATTC
CAACAAAGTTTGATTTTCTCTGTATTTTCTTACTTACTATGGGTTACATTTTATTTTT
CAAATTTGGATGATAATTTCTTGGAAACATTTTTTATGTTTTAGTAAACAGTATTTTTTTGT
GTTTCAAAGTGAAGTTTACTGAGAGATCCATCAAATGAACATCTGTTGTAATTTAAATTT
TTGGCCACTTTTTTCTAGATTTTACATCATTTCTGTCTGAACCTCAACTGAAATTTGTTTTTT
TTTCTTTTTGGATGTGAAGGTGAACATTTCTGATTTTGTCTGATGTGAAAAAGCCTTGGTA
TTTTACATTTTGA AAATTCAAAGAAGCTTAATATAAAAGTTTGCAATTTCTACTCAGGAAAAAG
CATCTTCTGTATATGCTTAAATGTATTTTGTCTCATATACAGAAAGTCTTAATTTGAT
TTTACAGTCTGTAATGCTGTGTTTTTAAATAATAACATTTTATATTTTTTAAAGACAA
ACTTCATATATCCTGTGTTCTTTCTGACTGGTAAATATTGTGTGGGATTTCACAGGTA
GTCAGTAGGATGGAACATTTTAGTGATTTTTTACTCTTAAAGAGCTAGAATACATAGTTTT
CACCTTAAAGAAGGGGAAAAATCATAAATCAATGAATCACTGACCATTACGTAGTAGAC
AATTTCTGTATATGCCCTTCTTCTAGGCTCTGTGCTGTGTGAATCCATTAGATTTACAG
TATCGTAATATACAAGTTTTCTTTAAAGCCCTCTCCTTTAGAATTTAAAAATTTGTACCAT
AAAGAGTTTGGATGTGAACCTGTGATGCTTGA AAAAATATCCTAAGCACAAAATAAACCT
TTCTAACCACTTCATTAAGCTGAAAAA

0904526 071304

FIGURE 114

MAPSGSLAVPLAVLVLLWGAPWTHGRRSNVRVITDENWRELLEGDWMIEFYAPWCPACQNL
QPEWESFAEWGEDLEVNIKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFI
NFISDKEWKSIEPVSSWFGPGSVLMSSMSALFQLSMWIRTCHNYFIEDLGLPVWGSYTVFAL
ATLFSGLLLGLCMIFVADCLCPSKRRRPQYPYPYPSKKLLSESAQPLKKVEEEQEADEEDVSE
EEAESKEGTNKDFPQNAIRQPSLGPSLATDKS

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 182-201

Casein kinase II phosphorylation site.

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

Tyrosine kinase phosphorylation site.

amino acids 107-115

N-myristoylation site.

amino acids 20-26, 192-198

Amidation site.

amino acids 25-29

FIGURE 115

GCGAGTGTCCAGCTGCGGAGACCCGTGATAATTCGTAACTAATTCACAAACGGGACCCTT
 CTGTGTGCCAGAAACCGCAGCAGTTGCTAACCCAGTGGGACAGGCGGATTGGAAGAGCGGG
 AAGGTCTGGCCCGAGCAGTGTGACACTTCCCTCTGTGACCAATGAAACTCTGGGTGTCTGC
 ATTGCTGATGGCCTGGTTTGGTGTCTGAGCTGTGTGCAGGCCGAATCTTCCACCTCTATTG
 GGCACATGACTGACCTGATTTATGCAGAGAAAGAGCTGGTGCAGTCTCTGAAAGAGTACATC
 CTTGTGGAGGAAGCCAAGCTTTCCAAGATTAAGAGCTGGGCCAACAAATGGAAGCCTTGAC
 TAGCAAGTCAGCTGCTGATGCTGAGGGCTACCTGGCTCACCTGTGAATGCCATACAACTGG
 TGAAGCGGCTAAACACAGACTGGCCTGCGCTGGAGACCTTGTCTGCAGGACTCAGTGCA
 GGTTTTATCGCCAACTCTCTGTGCAGCGGCAGTTCTTCCCCACTGATGAGGACGAGATAGG
 AGCTGCCAAAGCCCTGATGAGACTTCAGGACACATACAGGCTGGACCCAGGCACAATTTCCA
 GAGGGGAACCTCCAGGAACCAAGTACCAGGCAATGCTGAGTGTGGATGACTGCTTTGGGATG
 GGCCGCTCGGCCTACAATGAAGGGACTATTATCATAACGCTGTTGTGGATGGAGCAGGTGCT
 AAAGCAGCTTGATGCCGGGAGGAGGCCACCACAACCAAGTCACAGGTGCTGGACTACCTCA
 GCTATGCTGTCTTCCAGTTGGGTGATCTGCACCGTGCCCTGGAGCTCACCCGCCGCTGCTC
 TCCCTTGACCCAAAGCCACGAACGAGCTGGAGGGAATCTGCGGTACTTTGAGCAGTTATTGGA
 GGAAGAGAGAGAAAAACGTTAACAAATCAGACAGAAGCTGAGCTAGCAACCCAGAAAGCA
 TCTATGAGAGGCTGTGGACTACCTGCCTGAGAGGGATGTTTACGAGAGCCTCTGTGCTGGG
 GAGGGTGTCAAACCTGACACCCCGTAGACAGAAGAGGCTTTTCTGTAGGTACCACCATGGCAA
 CAGGGCCCCACAGCTGCTCATTTGCCCTTCAAAGAGGAGGACGAGTGGGACAGCCGCACA
 TCGTCAGGTACTACGATGTCTGCTGATGAGGAAATCGAGAGGATCAAGGAGATCGCAAAA
 CCTAAACTTGCAGGAGCCACCGTTCTGTGATCCAGACAGGAGTCCCTACTGTGCGCAGTA
 CCGGGTTTCCAAAAGCTCCTGGCTAGAGGAAGATGATGACCTGTTGTGGCCCGAGTAAATC
 GTCGGATGCAGCATATCACAGGGTTAAACAGTAAAGACTGCAGAATGTTTACAGGTTGCAAA
 TATGGAGTGGGAGGACAGTATGAACCGCACTTCGACTTCTCTAGGCGACCTTTTGACAGCGG
 CCTCAAAACAGAGGGGAATAGGTTAGCGACGTTTCTTAACATCAGTGAAGTGAAGAAGCTG
 GTGGTGCCACCGTCTTCCCTGATCTGGGGCTGCAATTTGGCCTAAGAAGGGTACAGCTGTG
 TTCTGGTACAACCTCTTGGGAGCGGGGAAGGTGACTACCGAACAAAGACATGCTGCTGCC
 TGTGCTTGTGGGCTGCAAGTGGGTCTCCAATAAGTGGTTCATGAACGAGGACAGGAGTTCT
 TGAGACCTTGTGGATCAACAGAAGTTGACTGACATCCTTTTCTGTCTTCCCTTCTCTGGTC
 CTTAGCCCATGTCTAACGTGACAGACACCTTTGTATGTTCCCTTGTATGTTCCATATCAGGCT
 GATTTTTGGAGAAATGAATGTTTGTCTGGAGCAGAGGGAGACCATACTAGGCGCATCTCCTGT
 GTGACTGAAGTCCAGCCCTTCCATTACAGCCTGTGCCATCCTGGCCCCCAAGGCTAGGATCA
 AAGTGGCTGCAGCAGAGTTAGCTGTCTAGCGCCTAGCAAGGTGCCCTTTGTACCTCAGGTGTT
 TTAGGTGTGAGATGTTTCAGTGAACCAAAGTTCTGATACCTTGTTTACATGTTTGTTTTAT
 GGCATTTCTATCTATTGTGGCTTTACCAAAAAATAAAATGTCCCTACCAGAAAAA

000433: 071304

FIGURE 116

MKLWVSALLMAWFGVLSVCVQAEFFTSIGHMTDLIYAEKELVQSLKEYILVEEAKLSKIKSWA
NKMEALTSKSAADAEGYL AHPVNAYKLVKRLNTDWPAL EDLVLQDS AAGFIANLSVQRQFFP
TDEDEIGAAKALMRLQD TYRLDPGTISR GELPGTKYQAMLSVDDCFGMGRSAYNEG DYYHTV
LWMEQVLKQLDAGEEATTTKSQVLDYLSYAVFQLGDLHRALELTRRLSLDPSHERAGGNLR
YFEQLLEEREKTLTNQTEAELATPEGIYERPV DYLPERDVYESLCRGE GVKLT PRRQKRLF
CRYHHGNRAPQLLIAPFK EEDWDSPHIVRY YDVMSDEEIERIKEI AKPKLARATVRDPKTG
VLTVASYRVSKSSWLEEDDDPVVARVNRRMQHITGLTVKTAE LLQVANYGVGGQYEPHFD FS
RRPFD SGLKTEGNRLATFLNYMSDVEAGGATVFPDLGAAIWPKKGTAVFWYNLLRSSEG DYR
TRHAACPVLVGCKWVSNKWFHERGQEFLRPCGSTEV D

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 115-119, 264-268

Glycosaminoglycan attachment site.

amino acids 490-494

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 477-481

Casein kinase II phosphorylation site.

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,
346-350, 365-369, 385-389, 457-461, 530-534

Tyrosine kinase phosphorylation site.

amino acids 71-80, 489-496

N-myristoylation site.

amino acids 14-20, 131-137, 171-177, 446-452

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 8-19

Leucine zipper pattern.

amino acids 213-235

[illegible]

CCAGATTGATGAGTTTACTTTCTCTCTCTTTTATGTGGAGACAGACAATAATCCAGGTGTGAGTGAATTTGATTGT
TTCATTATTACACTTTTGGCTTGGGGTGTAGTTTCGCACACTTCACAGTTCGAGAGACGACAGAGAGTTGTGA
AGACAGACCACTCTTCTGGGATGCTGCTGTCGGAAGCCAGCGGGCTTCTGTCTGTCTTGGCTCATGTGACCC
CAGGTTTCTCTGGTTAAATCTGAAGCCCTACTATCTGGCTTGTGTCCTCAATTCATGTATCTTGAGGCTGTGCC
CTGGGGACCCACCTGGGACGGGCTACCACTAGCAGCTAGAGTCCCTGTTGGCTGTCTGTGGGACGAGCTCT
CCCTCATCTTAGGGCTGTCTCTGGGGTGCAGCTAGAGCTCTCGGGGTTCTCTGGATACAGGGGGAGGGAGAG
ATCCCTGTGTGCAGGGCTGTAGGGAGCGGAGGAGGGCCACAGAATCCAGATTGCAGAGCTGGGTACGCCAAAGT
ATGAAGACTTCAAAACCCGGATTTGTCCTCTACTACAGGAGGCCCAACAGAGCTACAAAGAGGTGTCTCAGAGCT
GGTACATCCAGACAGAGCTTGGGCTCCGATGAGCGGTGTCTGGTGGCTGTCTCTGATCCCTCCGAGCTACACTGTCCA
CTTTGGCGTGGCTGTGAACCGTGGTGGCGCCCATCTCTCCGGTACTTACTTCTATCTGGGACGCGGGGG
CCGGGCTGTGCAGAGGATGTGAGGTGTGTCTATGGGATAGAGCGGCGGCTGCTCATGTGCAGAGACCGCTGC
GCCACTCTCACACACTTTTGGGGCCGACATACAGCTGGTTCCTCATCATCAGGAGTGAACATATGTGTGACGGCCC
CCCGCTGGACGCCCTTGTCTGGCCACTCAGACTCAACAGAGCTGTACTTAGGCGGGCAGAGAGGTTCATTGT
GGCAGCGGACGAGCGGCCGATGTCTATGGGGGCTTTGGCTACCTGTGCTGATCCAGGAGTCTCTGCTCTGTCTGC
GGCCACTCTGGATGGCTCGCAGGAGACATCTCAGTGGCCGTCTGACGAGTGGCTTGGACGCTGCCCTCATTTG
ACTCTTGGGCGTGGCTGTGTCTACAGACAGGGGCGACAGTACGCTATGAACTGGCCACAAATTAAGG
ACCTTGAGAGGAGAGGAGCTCGGCTTTCTTGAGTGGCTTCGCGCTGACACCTGTCTCGAAGAGTCCCTCATGT
ACCGGCTGCACAAACGCTTCACGCTCTTGAGTGTGGAGCGGGCTAGAGTGAATATGACAACTCTCAGGCTCAGA
TCCGAAACTCGACGTGTCCAGCCCGAAGGGAGCGAGCTGAGCTGGCCGCTTGGGCTCCCTGCTCTTCTCA
TACCACACTCTCGCTTTGAGGTGCTTGGCTGGGACTACTTACAGACGACCACTCTTCTGTTCGAGATGGGG
CTCCACAGTGGCCACTTACAGGGGGCTAGCAGGGGCGAGCTGGTGATCTGGAGACTGCCCTGGAGCAGCTCA
ATCGGCGTTCACGACCCGCTCGCTCTTCAGAGCAGCAGCTGTCAACGGCTATCGGCGCTTCGACCCAGCAC
GGGACAGGAGTACACCTTGGACTGCTGTGTGGAATTTGTGACACAGAGCTGGGACCGGGCGGCTCGGCTCGCA
GGGTGACCTGCTGGCGCACAGGCGGGGTGGAATCTCACTATGGCTATGTCACTAGAGCGCACTCCAGGTGCT
AGCTGTGTCTGCACCTCTGGTGTGAGGCTGTGACGACCGGCGCTTTCTCTCGAGGCTTTTGCAGCAATGTGC
TGAGGACACAGAAACTGTAGTGTCTACCTCTGTCTGGTCTACGGGCAACAGAAAGTGGCGTGGAGCTCAG
ACCCATTTCTGGGGTGAAGGCTGCAGCAGCGGAGTTAGAGCGACGGTACCTGGGACAGGGCTGGCTGCTCTCG
CTGTGCGACAGAGGCCCTCCAGAGTGGCATCATGTGAGTGTCTGAGAAAGACCTCTTGGACATCTCTCT
CTTTCTTACCAACGCTGTGGAACAGGCTGGGGCGAAGTCCCAACCGCTGTGCATGAATGGCTCTTTGGCT
GGCAGGCTCTTCTTTCAGTGTGATTTTCAGAGATTTCAATCTGCCCTTACACAGAGATACCCACCGGCGCCC
CGGGGGTGGCCCTTCAACCCCCCTCCCCCTGGTGTGACCCCTCCCGGGGGGCTCTTATGGGGGGAGATTG
ACCGGACGCTTTCTGGAGGGGCTGCTTCTACACGCTGACTCTCTGGCGGGCAGCGCGGCTGGAGGTGAAC
TGGCAGGTCGAGGAAGAGGAGGAGCCCTGGAGGGGCTGGAGGTGATGGAATGTCTTCTCTCGGTTCTCAGGCTCA
ACCTCTTTGGGCGCTAGAGCAGGCTGGTGCAGAGTTCTCTCCCTCGAGAGTCAAGCCAGCGCTCAGTGAAG
AATCTTACCAACGCTCGGCCCTCAGCACACTGAGGAGGGCTAGAGGGCGCTGCCACGCTTGGCTATGGCTCTTTTG
ACGAGGAGAGGCGCAATAGACTTAGCCGCGCTGGGGCGCTAACTCATTAATCTTTCTTTGTCTGCTCAGCG
CCAGGAAGGCGAGGCAAGATGGTGGACAGATAGAGAATTTGTGCTGATATTTTAAATATGAAATGTTTAA
ACATGTTCTCTTGCC

FIGURE 118

MRLSSLLALLRPALPLILGLSLGCSLSLLRVSWIQEGEDPCVEAVGERGGPQNPD SARLD
QSD E D F K P R I V P Y Y R D P N K P Y K K V L R T R Y I Q T E L G S R E R L L V A V L T S R A T L S T L A V A V N R T V
A H F F P R L L Y F T G Q R G A R A P A G M Q V V S H G D E R P A W L M S E T L R H L H T F G A D Y D W F F I M Q D D T Y
V Q A P R L A A L A G H L S I N Q D L Y L G R A E E F I G A G E Q A R Y C H G G F G Y L L S R S L L R L R P H L D G C R G
D I L S A R P D E W L G R C L I D S L G V G C V S Q H Q G Q Q Y R S F E L A K N R D P E K E G S S A F L S A F A V H P V S E
G T L M Y R L H K R F S A L E L E R A Y S E I E Q L Q A Q I R N L T V L T P E G E A G L S W P V G L P A P F T P H S R F E V
L G W D Y F T E Q H T F S C A D G A P K C P L Q G A S R A D V G D A L E T A L E Q L N R R Y Q P R L R F Q K Q R L L N G Y R
R F D P A R G M E Y T L D L L L E C V T Q R G H R R A L A R R V S L L R P L S R V E I L P M P Y V T E A T R V Q L V L P L L
V A E A A A A P A F L E A F A A N V L E P R E H A L L T L L L V Y G P R E G G R G A P D P F L G V K A A A A E L E R R Y P G
T R L A W L A V R A E A P S Q V R L M D V V S K K H P V D T L F F L T T V W T R P G P E V L N R C R M N A I S G W Q A F F P
V H F Q E F N P A L S P Q R S P P G P P G A G P D P P S P P G A D P S R G A P I G G R F D R Q A S A E G C F Y N A D Y L A A
R A R L A G E L A G Q E E E E A L E G L E V M D V F L R F S G L H L F R A V E P G L V Q K F S L R D C S P R L S E E L Y H R
C R L S N L E G L G G R A Q L A M A L F E Q E Q A N S T

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 489-507

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-68, 150-154, 322-326, 331-337, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-678

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 119

CGGAGTGGTGCGCCAACGTGAGAGGAAACCCGTGCGGGCTGCGCTTTCCTGTCCCCAAGCC
GTTCTAGACGCGGGAAAAATGCTTTCTGAAAGCAGCTCCTTTTGAAGGGTGTGATGCTTGG
AAGCATTTTCTGTGCTTTGATCACTATGCTAGGACACATTAGGATTGGTCATGGAAATAGAA
TGCACCACCATGAGCATCATCACCTACAAGCTCCTAACAAAGAAGATATCTTGAAAATTCA
GAGGATGAGCGCATGGAGCTCAGTAAGAGCTTTCGAGTATACTGTATTATCCTTGTA AAC
CAAAGATGTGAGTCTTTGGGCTGCAGTAAAGGAGACTTGGACCAAACACTGTGACAAAAGCAG
AGTTCTTCAGTTCTGAAAATGTTAAAGTGTTCAGTCAATTAATATGGACACAAATGACATG
TGGTTAATGATGAGAAAAGCTTACAAATACGCCCTTTGATAAGTATAGAGACCAATACAACCTG
GTTCTTCCTTGACGCGCCCACTACGTTTGCTATCATTGAAAACCTAAAGTATTTTTTGTAA
AAAAGGATCCATCAGACGCTTTCTATCTAGGCCACACTATAAAATCTGGAGACCTTGAATAT
GTGGGTATGGAAGGAGGAATTGTCTTAAGTGTAGAATCAATGAAAAGACTTAACAGCCTTCT
CAATATCCCAGAAAAGTGTCCTGAACAGGGAGGGATGATTGGAAGATATCTGAAGATAAAC
AGCTAGCAGTTTGCCCTGAAATATGCTGGAGTATTTGCAGAAAATGCAGAAGATGCTGATGGA
AAAGATGTATTTAATACCAAATCTGTTGGGCTTTCTATTAAAGAGGCAATGACTTATCACCC
CAACCAGGTAGTAGAAGGCTGTTGTTTCAGATATGGCTGTTACTTTTTAATGGACTGACTCCAA
ATCAGATGCATGTGATGATGTATGGGGTATACCGCCTTAGGGCATTGGGCATATTTTCAAT
GATGCATGGTTTTCTTACCTCCAAATGGTTCTGACAATGACTGAGAAGTGGTAGAAAAGCG
TGAATATGATCTTTGTATAGGACGTGTGTTGTGTCATTATTTGTAGTAGTAACACATATCCAA
TACAGCTGTATGTTCTTTTCTTTCTAATTTGGTGGCAGTGGTATAACCACACATTAAAG
TCAGTAGTACATTTTAAATGAGGGTGGTTTTTTTCTTTAAACACATGAACATTGTAAATG
TGTGGAAAAGAGTGTTTTAAGAATAATAATTTGCAAATAAACTATTAATAAATATTATAT
GTGATAAATCTAAATTATGAACATTAGAAATCTGTGGGGCACATATTTTGTCTGATTGGTT
AAAAAATTTTAAACAGGTCTTTAGCGTTCTAAGATATGCAAATGATATCTCTAGTTGTGAATT
TGTGATTAAAGTAAACCTTTAGCTGTGTGTTCCCTTTACTTCTAATACTGATTATGTCTC
AAGCCTCCCCAAGTTCATGGATTGCGCTTCTCAAAATGTACAACCTAAGCAACTAAAGAAA
ATTAAAGTGAAAGTTGAAAAAT

FIGURE 120

MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISEDERME
LSKSFRVYCIILVKPKDVSLSWAAVKETWTXKCDKAEFFSSENVKVFESINMDTNDMWLMMRK
AYKYAFDKYRDQYNWFFLARPTTFAIENLKYFLKKDPSQPFYLGHTIKSGDLEYVGMEGG
IVLSVESMKRLNSLLNIPEKCPQGGMWIKISEDKQLAVCLKYAGVFAENAEDADGKDVFNT
KSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMYGVYRLRAFGHIFNDALVFL
PPNGSDND

Signal sequence:

amino acids 1-33

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-672

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 121

CCCACGCGTCCGATCTTACCAACAAAACACTCCTGAGGAGAAAGAAAAGAGAGGGAGGGAGAG
AAAAAGAGAGAGAGAGAGAAAACAAAAACCAAAGAGAGAGAAAAAATGAATTTCATCTAAATCAT
CTGAAACACAATGCACAGAGAGAGGATGCTTCTCTTCCCAAATGTTCTTATGGACTGTTGCT
GGGATCCCCATCCTATTTCTCAGTGCCTGTTTCATCACCAGATGTGTTGTGACATTTTCGCAT
CTTTCAAACCTGTGATGAGAAAAAGTTTCAGCTACCTGAGAATTTACAGAGCTCTCCTGCT
ACAATTATGGATCAGGTTCAAGTCAAGAATTGTTGTCCATTGAACTGGGAATATTTTCAATCC
AGCTGCTACTTCTTTTCTACTGACACCATTTCCTGGGCGTTAAGTTTAAAGAACTGCTCAGC
CATGGGGGCTCACCTGGTGGTTATCAACTCACAGGAGGAGCAGGAATTCCTTTCCTACAAGA
AACCTAAAAATGAGAGAGTTTTTTATTGGACTGTCAGACCAGGTTGTCGAGGGTCAGTGGCAA
TGGGTGGACGGCACACCTTTGACAAAGTCTCTGAGCTTCTGGGATGTAGGGGAGCCCAACAA
CATAGCTACCTGGAGGACTGTGCCACCATGAGAGACTCTTCAAACCCAAGGCAAAATTGGA
ATGATGTAACCTGTTTCCTCAATTATTTTCGGATTTGTGAAATGGTAGGAATAAATCCTTTG
AACAAAGGAAAATCTCTTTAAGAACAGAAAGGCACAACCTCAAATGTGTAAAGAAGGAAGAGCA
AGAACATGGCCACACCCACCGCCCCACACGAGAAATTTGTGCGCTGAACTTCAAAGGACTTC
ATAAGTATTTGTTACTCTGATACAAATAAAAATAAGTAGTTTAAATGTTAAAAA
AA
AAAAA

FIGURE 122

MNSSKSSETQCTERGCFSSQMFLWTVAGIPILFLSACFITRCVVTFRIFQTCDEKKFQLPEN
FTELSYCYNYGSGSVKNCCPLNWEYFQSSCYFFSTDTISWALSLSKNC SAMGAHLVVINSQEEQ
EFLSYKKPKMREFFIGLSDQVVEGQWQWVDGTPLTKSLSFWDVGEPNNIATLEDCATMRDSS
NPRQNWNDVTCFLNYFRICEMVGINPLNKGKSL

Signal sequence:

amino acids 1-42

N-glycosylation site.

amino acids 2-6, 62-66, 107-111

Casein kinase II phosphorylation site.

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

N-myristoylation site.

amino acids 15-21, 74-80, 155-161

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 27-38

FIGURE 123

GGGACTACAAGCGCGCGCGCTGCCGCTGGCCCTCAGCAACCCCTGCAGATGGCGCTGAGGCGGCCACCGCGAC
TCCGGCTCTCGCTCGGCTGCCTGACTTCTTCTGCTGCTGCTTTTCAGGGGCTGCCTGATAGGGGCTGTAAATC
TCAAAATCCAGCAATCGAACCCAGTGTGTACAGGAATTTGAAAGTGTGGAACGTGCTTGCATCAATTACGGATTGCG
AGACAAGTGACCCAGGATCGAGTGGGAAGAAAATTCAGAGTGAACAAACCAATATGTGTTTTTGACACCAAAA
TTGAGGGAGACTTGGCGGGTCTGTCAGAAATCTGGGGAAGACATCCCTGAAGATCTTGGAAATGTGACACCGAGAG
ACTCAGCCCTTTATCGCTGTGAGGTCGTGTCTGAAATGACCGCAAGGAAATGTATGAGATTGTGATCGATTAA
CTGTGCAAGTGAAGCGTGAACCCCTGTCTGTAGAGTGCAGAGGCTTACCAAGTAGGCAAGATGGCAACACTGC
ACTGCCAGGAGAGGTGAGGGCCACCCCGGCTCACTACAGCTGGTATCGCAATGATGTACACTGCCACGGATT
CCAGAGCCAAATCCGATTTTCGCAATCTCTTTCCACTTAAACTCTGAAACAGGCGACTTGGTGTCTCACTGCTG
TTCACAGGACGACTCTGGGCACTACTACTGCAATGCTTCCAATGACGAGGCTCAGCCAGGTGTGAGGAGCAGG
AGATGGAAGTCTATGACCTGAACATTGGCGGAATTTATGGGGGGTTCGTGTGCTGTCTGCTGTCTGGCCCTGA
TCACGTTGGGCATCTGCTGTGCATACAGACGTGGCTACTTTCATCAACAATAAAGCAGGATGGAGAAAGTTACAAGA
ACCCAGGGAACAGATGGAGTTAACTACATCCGACTGACGAGGAGGGCGACTTCAGACACAAGTCACTGCTTTG
TGATCTGAAGCCCGCGTGTGGCTGAGAGCGCAGACGCGCAGTGCACATACCTGTCTAGAAACTCCTGTCAA
GGCAGCGAGAGCTGATGCATCGACGAGCTAGACACTCATTAGAAGCTTTTCGTTTTGGCCAAAGTTGACCA
CTACTCTTTTACTTAACAAAGCCACTGAATAGAAGATTTTCTCAAGATGGAACCGGTAAATAAACCACAA
GGAAGCGAAACTGGTGGCTTCACTGAGTTGGGTTCTTAATCTGTTTCTGGCTGATTCCCGCATGAGTATTGG
GTGATCTTAAAGAGTTTGTCTCAGTAAACGCCGCTGCTGGGCCCTGTGAAGCAGCATGTTCACCACTGGTCTGT
CAGCAGCCACGACGACCATGTGAGATGGCGAGGTGGCTGGACAGCACCAGCAGGCTTCTTCTTAAAGGCTCTGC
GAAAAGGCTTCTTACACGAGCCCTTACTTCTCGGCCACAGACACCCAGCTTCTTCTTAAAGGCTCTGC
TGATCGGTTGTCAGTGTCCATTGTGGGAGAAGCTTTTGGATCAGCATTTGTAAAAACACCAAATCAGGAAG
GTAAATTGGTGTCTGGAAGAGGATCTTGCTGAGGAACCTGCTTGTCCAAAGGCTGTCAAGATTTAAGGAAA
ACCTTCGCTTAGGCTAAGCTGAAATGGTACTGAAATATGCTTTTCTATGGGTCTTGTATTATTTATAAAATTT
TACATCTAAATTTTGTCTAAGGATGTATTTTGATTTATGAAAAGAAAATTTCTATTTAAACTGTAATATATTGT
CATACAATGTAAATAACCTATTTTTTAAAAAAGTTCAACTTAAGGTAGAAGTTTCAAGCTACTAGTGTAAAT
TGGAAAAATACAATAATTAAAGATTTTACCCAAGGAATCTCTCATGGAAGTTTACTGTAGTGTCTCTTTCT
CACACAAGTTTAGCCTTTTTCACAGGGAATCACTACTGTCTACACATCAGACCATAGTTGCTTAGGAAACCTT
TAAAAAATTCAGTTAAGCAATGTTGAAATCAGTTTGCATCTCTTCAAAAGAAAATCTCAGGTTAGCTTTGAACT
GCCTCTTCTGAGATGACTAGGACAGTCTGTACCAGAGGCCACCCAGAAGCCCTCAGATGTACATACAGAGTG
CCAGTCAGCTCTGGGGTGTGCGCAGGCGCCCGCTCTAGCTCACTGTGTCCTGCTGTCTGCCAGGAGGCCCT
GCCATCTCTGGGCCCTGGCAGTGGCTGTGTCCCAGTGAGCTTTACTACGTGGCCCTTGTCTCATCCAGCACAGC
TCTCAGGTGGGCATGCAAGGACACTGGTGTCTTCCATGTAGCGTCCAGCTTTGGGCTCCTGTACACAGACCTCT
TTTTGGTTATGGATGGCTCAAAAATAGGGCCCCCAATGCTATTTTTTTTTTTAAAGTTTGTATTATTTGTT
AAGATTGTCTAAGGCCCAAAGGCAATTCGAAATCAAGCTCTGTCAAGTACAATAAATTTTAAAAAGAAAATGGAT
CCCACTGTCTCTCTTGTGCCACAGAGAAAGCACCCAGACGCCACAGGCTCTGTGCGATTTTCAAAACAAACCATGAT
GGAGTGTGCGGCCAGTCCAGCCTTTTAAAGAACGTGAGGTGGAGCAGCAGGAGTGAAGGCCCTGGCGGGGAGGAAAG
TGAAACGCCGTAATCAAAGCAGTTTCTAATTTTGAATTTTAAATTTTTCATCGCGCGGAGACATGTCTCCATTT
TGTGGGGGGACATTAGCAACATCACTCAGAAGCCTGTGTTCTTCAAGAGCAGGTGTTCTCAGCCTCAGATGCCCT
GCCGTTCTGAGCTCAGGACTGAAGTGCTGTAAAGCAAGGAGCTGCTGAGAAGGAGCACTCCACTGTGTGCGCTGGA
GAATGGCTCTCACTACTCACCCTGTCTTTCAGCTTCCAGTGTCTTGGGTTTTTATACCTTTGACAGCTTTTTTTT
AATTGCTATACATGAGACTGTGTTGACTTTTTTAGTTATGTGAACACACTTTGCGCAGGCCGCTGGCAGAGGCA
GGAATGCTCCAGAGTGGCTCAGTCTCCCTGGTCTGTGCTGATGGCATGCTATGCTTACGATGCAAGTTTC
CTCTCAATCATGTCCACCTTGGTAGAGGGGATGGCTCCCCACCTCAGCGTTGGGGATTCAAGCTCCAGCTCTCT
TCTTGGTTCTATAGTATAGGTAGGCTTATTGCCCCCTCTTCTATACCTTCAAACTTCTACACTAGTGCCA
TGGGAACAGGCTGTGAAAGAGTAGAGAGAAGTGAAGTAGAGTCTGGGAAGTAGCTGCTTAACTAGACAGTAGA
CGGAAAGGAATCTCTGTGTTATTTAGATATGAATGTGACTCAAGACTGAGGCCGATCAGGCTGTGATCTCT
GCCCTTGGATGAGTGTGCTGTACACAGATGCTACAGACTTGTACTAACACCCGTAATTTGGCATTGTTTAACT
CTCATTTATAAAGCTTCAAAAAACCA

0990423-07304

FIGURE 124

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624
><subunit 1 of 1, 310 aa, 1 stop
><MW: 35020, pI: 7.90, NX(S/T): 3
MALRRPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVQVEFESVELSCIITDSQTS
PRIEWKKIQDEQTTTVFFDNKIQGDLAGRAEILGKTSLSKIWNVTRRDSALYRCEVVARNDRK
EIDEIVIBLTVQVKPVTVPVCRVPAVPGKMATLHCQSESEGHPRPHYSWYRNDVPLPTDSRA
NPRFRNSSFFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEYVDLNIIGGIIG
VLVVLAVLALITLIGICCAYYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI

Important features of the protein:

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 243-263

N-glycosylation sites.

amino acids 104-107, 192-195

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 107-110

Casein kinase II phosphorylation site.

amino acids 106-109, 296-299

Tyrosine kinase phosphorylation site.

amino acids 69-77

N-myristoylation sites.

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267